

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:34:18 ; Search time 150.545 Seconds
(without alignments)
70.046 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHNQEVTAEDGTQAEKSKPCA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	24	4	AAB68627
2	132	100.0	47	4	AAB68665
3	128	97.0	24	4	AAB68663
4	128	97.0	387	9	ADZ47819
5	128	97.0	402	7	ADM29354
6	128	97.0	419	4	AAE09203
7	128	97.0	419	4	AAE09211
8	128	97.0	419	4	AAE09210
9	128	97.0	419	4	AAE09205
10	128	97.0	419	4	AAE09208
11	128	97.0	419	4	AAE09206
12	128	97.0	419	4	AAE09207
13	128	97.0	419	4	AAE09213
14	128	97.0	419	4	AAE09202
15	128	97.0	419	4	AAE09214
16	128	97.0	419	4	AAE09212
17	128	97.0	419	4	AAE09215
18	128	97.0	419	4	AAE09216
19	128	97.0	419	4	AAE09181
20	128	97.0	419	4	AAE09183
21	128	97.0	419	4	AAE09200
22	128	97.0	419	4	AAE09204
23	128	97.0	419	4	AAE09209
24	128	97.0	419	5	AAE20348

251	128	97.0	419	7	ADFI6709	Adfi6709 Human alb
26	128	97.0	419	9	ADY28119	Ady28119 Receptor
27	128	97.0	419	9	ADZ47861	Adz47861 Wild-type
28	128	97.0	420	3	AAV97240	Aay97240 Truncated
29	128	97.0	509	6	AAE36793	Aae36793 Human Erb
30	128	97.0	509	8	ADN12292	Adn12292 Human Erb
31	128	97.0	575	8	ADT50878	Adt50878 Cancer re
32	128	97.0	575	9	ADY28117	Ady28117 Receptor
33	128	97.0	575	9	ADZ47797	Adz47797 Amino aci
34	128	97.0	614	9	ADZ47809	Adz47809 Amino aci
35	128	97.0	624	2	AAR08222	Aar08222 Extracell
36	128	97.0	633	9	ADY28116	Ady28116 Receptor
37	128	97.0	633	9	ADZ47862	Adz47862 Human 100
38	128	97.0	645	4	AAB60408	Aab60408 Human Erb
39	128	97.0	645	4	AAB61593	Aab61593 Human Erb
40	128	97.0	645	5	ABG70753	Abg70753 Human HER
41	128	97.0	645	8	ADE71462	Ade71462 Human Erb
42	128	97.0	645	8	ADJ88016	Adj88016 Human Erb
43	128	97.0	645	8	ADP43330	Adp43330 Extracell
44	128	97.0	653	3	AAB21200	Aab21200 Extracell
45	128	97.0	653	5	AAM51145	Aam51145 Human Her
46	128	97.0	675	9	ADM87401	Adm87401 Human cod
47	128	97.0	678	8	ADT50884	Adt50884 Cancer re
48	128	97.0	678	9	ADZ47795	Adz47795 Amino aci
49	128	97.0	680	9	ADY28115	Ady28115 Receptor
50	128	97.0	685	7	ADG17938	Adg17938 Human HER
51	128	97.0	690	7	ADG17945	Adg17945 Extracell
52	128	97.0	696	9	ADW28504	Adw28504 Human HER
53	128	97.0	712	3	AAB21204	Aab21204 Human HER
54	128	97.0	712	5	AAM51149	Aam51149 Her-2/neu
55	128	97.0	715	7	ADG17944	Adg17944 Human HER
56	128	97.0	717	9	ADZ47807	Adz47807 Amino aci
57	128	97.0	720	7	ADG17940	Adg17940 Human HER
58	128	97.0	741	7	ADM29356	Adm29356 Human nov
59	128	97.0	782	2	AAW19764	Aaw19764 Her2-QM-C
60	128	97.0	919	3	AAB21203	Aab21203 Human HER
61	128	97.0	919	5	AAM51148	Aam51148 Her-2/neu
62	128	97.0	951	3	AAV44993	Aay44993 DC8scfv-e
63	128	97.0	960	9	ADY30513	Ady30513 Human spl
64	128	97.0	1006	7	ADFI6546	Adfi6546 Human alb
65	128	97.0	1042	7	ADM29352	Adm29352 Human nov
66	128	97.0	1200	3	AAB21208	Aab21208 Human HER
67	128	97.0	1217	8	ADT50876	Adt50876 Cancer re
68	128	97.0	1223	5	Aau98923	Aau98923 Human bre
69	128	97.0	1253	7	ADC35106	Adc35106 Human bre
70	128	97.0	1255	2	AAW01111	Aaw01111 HER-2/neu
71	128	97.0	1255	3	AAV92620	Aay92620 Human her
72	128	97.0	1255	3	AAV84780	Aay84780 Amino aci
73	128	97.0	1255	3	AAB21198	Aab21198 Human HER
74	128	97.0	1255	4	AAB60167	Aab60167 HER2 tran
75	128	97.0	1255	4	AAG88267	Aag88267 HER2/neu
76	128	97.0	1255	4	AAE12130	Aae12130 Human tyr
77	128	97.0	1255	4	AAB85458	Aab85458 Human HER
78	128	97.0	1255	5	AAE20479	Aae20479 Human Her
79	128	97.0	1255	5	AAU77114	Aau77114 Human Her
80	128	97.0	1255	5	AAE26349	Aae26349 Human HER
81	128	97.0	1255	5	AAE26366	Aae26366 Human HER
82	128	97.0	1255	5	AAU74545	Aau74545 Human HER
83	128	97.0	1255	5	AAM51143	Aam51143 Human Her
84	128	97.0	1255	5	AAE24067	Aae24067 Human Her
85	128	97.0	1255	6	ABR47447	Abra47447 Breast ca
86	128	97.0	1255	6	ABP74708	Abp74708 Human Her
87	128	97.0	1255	6	ABR43687	Abra43687 Human c-e
88	128	97.0	1255	6	AAE38390	Aae38390 Human c-e
89	128	97.0	1255	6	ADA38143	Ada38143 Human erb
90	128	97.0	1255	7	ADA37255	Ada37255 Human Erb
91	128	97.0	1255	7	ADBR2066	Adbr2066 Human Her
92	128	97.0	1255	7	ADB67621	Adb67621 Human epi
93	128	97.0	1255	7	ADC09593	Adc09593 Her2/Neu
94	128	97.0	1255	7	ADD25484	Add25484 Binding d
95	128	97.0	1255	7	ADG63281	Adg63281 Human Pro
96	128	97.0	1255	7	ADG63281	Adg63281 Human Pro
97	128	97.0	1255	7	ADG63281	Adg63281 Human Pro

98 128 97.0 1255 7 ADF45048 Adf45048 Human kin
99 128 97.0 1255 8 ADH13187 Adh13187 Human mal
100 128 97.0 1255 8 ADJ66554 Adj66554 Her2 prot

ALIGNMENTS

RESULT 1

AAB68627

ID AAB68627 standard; peptide; 24 AA.

XX AC AAB68627;

XX DT 30-APR-2001 (first entry)

XX DE HER-2 B cell epitope #6.

XX KW Cytostatic; immune response; HER-2; human; epitope; cancer; breast;
XX KW ovarian; lung; prostate; colon.
XX OS Homo sapiens.

XX PN WO200108636-A2.

XX PD 08-FEB-2001.

XX PF 03-AUG-2000; 2000WO-US021222.

XX PR 03-AUG-1999; 99US-0146869P.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Kaumaya PT, Stevens VC, Triozzi PL;

XX DR WPI; 2001-182849/18.

XX CC Compositions comprising polypeptides and polynucleotides for stimulating the immune system and for treating malignancies associated with overexpression of the HER-2 protein.
XX PT the immune system and for treating malignancies associated with overexpression of the HER-2 protein.
XX PS Claim 1; Page 37; 5lpp; English.

XX CC The present invention relates to compositions for stimulating the immune system and for treating malignancies associated with overexpression of the HER-2 protein. The compositions comprise immunogenic groups of the HER-2 proteins. The present sequence is one such peptide used in the compositions of the present invention. The compositions can be used for treating cancer, e.g. breast, ovarian, lung, prostate and colon cancers
XX SQ Sequence 24 AA;

Query Match 100.0%; Score 132; DB 4; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.3e-13;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPCA 24

Db 1 PLHNQEVTAEDGTQRAEKCKPCA 24

RESULT 2

AAB68665

ID AAB68665 standard; peptide; 47 AA.

XX AC AAB68665;

XX DT 30-APR-2001 (first entry)

XX DE HER-2 B cell epitope #15.

XX KW Cytostatic; immune response; HER-2; human; epitope; cancer; breast;
XX KW ovarian; lung; prostate; colon.

XX OS Unidentified.
XX PN WO200108636-A2.
XX PD 08-FEB-2001.
XX PF 03-AUG-2000; 2000WO-US021222.
XX PR 03-AUG-1999; 99US-0146869P.
XX PA (OHIS) UNIV OHIO STATE.
XX PI Kaumaya PT, Stevens VC, Triozzi PL;
XX DR WPI; 2001-182849/18.
XX CC Compositions comprising polypeptides and polynucleotides for stimulating the immune system and for treating malignancies associated with overexpression of the HER-2 protein.
XX PS Example 9; Page 31; 5lpp; English.
XX CC The present invention relates to compositions for stimulating the immune system and for treating malignancies associated with overexpression of the HER-2 protein. The compositions comprise immunogenic groups of the HER-2 proteins. The present sequence is one such peptide used in the compositions of the present invention. The compositions can be used for treating cancer, e.g. breast, ovarian, lung, prostate and colon cancers
XX SQ Sequence 47 AA;

Query Match 100.0%; Score 132; DB 4; Length 47;

Best Local Similarity 100.0%; Pred. No. 1.6e-12;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPCA 24

Db 1 PLHNQEVTAEDGTQRAEKCKPCA 24

RESULT 3

AAB68663

ID AAB68663 standard; peptide; 24 AA.

XX AC AAB68663;

XX DT 30-APR-2001 (first entry)

XX DE HER-2 B cell epitope #13.

XX KW Cytostatic; immune response; HER-2; human; epitope; cancer; breast;
XX KW ovarian; lung; prostate; colon.
XX OS Unidentified.

XX PN WO200108636-A2.

XX PD 08-FEB-2001.

XX PF 03-AUG-2000; 2000WO-US021222.

XX PR 03-AUG-1999; 99US-0146869P.

XX PA (OHIS) UNIV OHIO STATE.

XX PI Kaumaya PT, Stevens VC, Triozzi PL;

XX DR WPI; 2001-182849/18.

XX CC Compositions comprising polypeptides and polynucleotides for stimulating the immune system and for treating malignancies associated with overexpression of the HER-2 protein.

XX
PS Example 8; Page 30; 51pp; English.
XX
CC The present invention relates to compositions for stimulating the immune
CC system and for treating malignancies associated with overexpression of
CC the HER-2 protein. The compositions comprise immunogenic groups of the
CC HER-2 proteins. The present sequence is one such peptide used in the
CC compositions of the present invention. The compositions can be used for
CC treating cancer, e.g. breast, ovarian, lung, prostate and colon cancers
XX
SQ Sequence 24 AA;

Query Match 97.0%; Score 128; DB 4; Length 24;
Best Local Similarity 95.8%; Pred. No. 3e-12;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
|||||

RESULT 4
ADZ47819
ID ADZ47819 standard; protein; 387 AA.
XX
AC ADZ47819;
XX
DT 30-JUN-2005 (first entry)
XX
DE Amino acid sequence for human ErbB-2 variant VI.
XX
KW epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2005033133-A2.
XX
PD 14-APR-2005.
XX
PF 04-OCT-2004; 2004WO-US030903.
XX
PR 03-OCT-2003; 2003US-0507953P.
PR 10-NOV-2003; 2003US-0518321P.
PR 09-AUG-2004; 2004US-0599583P.
PR 07-SEP-2004; 2004US-0607326P.
XX
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
XX
PI Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX
WPI; 2005-285403/29.
DR N-PSDB; ADZ47818.
XX
PT New isolated polynucleotide encoding at least an active portion of an
PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
PT aberrant expression or activity of the ErbB-2 polypeptides, such as
PT cancer.
XX
PS Claim 42; SEQ ID NO 26; 246pp; English.
XX
CC The invention relates to the isolation of polynucleotide sequences
CC encoding novel epidermal growth factor receptor-2 (ErbB-2), also known as
CC HER-2 or neu polypeptides. Also described are methods, compositions, and
CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
CC treatment of ErbB-2 related cancer. The sequences, methods, and
CC compositions of the present invention are useful for diagnosing,
CC prognosing, and/or treating diseases or conditions associated with
CC aberrant expression or activity of the ErbB-2 polypeptides, such as
CC cancer. This sequence represents human ErbB-2 variant VI.
XX

SQ Sequence 387 AA;

Query Match 97.0%; Score 128; DB 9; Length 387;
Best Local Similarity 95.8%; Pred. No. 6.7e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339
|||||

RESULT 5
ADM29354
ID ADM29354 standard; protein; 402 AA.
XX
AC ADM29354;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human novel protein NOV20b.
XX
KW human; novel protein; NOV; cancer; immune associated disorder.
XX
OS Homo sapiens.
XX
PN WO2003064628-A2.
XX
PD 07-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-US003401.
XX
PR 01-FEB-2002; 2002US-0353287P.
PR 01-FEB-2002; 2002US-0353301P.
PR 12-FEB-2002; 2002US-0356371P.
PR 12-FEB-2002; 2002US-0356424P.
PR 13-FEB-2002; 2002US-0356531P.
PR 20-FEB-2002; 2002US-0358239P.
PR 26-FEB-2002; 2002US-0359603P.
PR 27-FEB-2002; 2002US-0359848P.
PR 27-FEB-2002; 2002US-0359860P.
PR 15-MAR-2002; 2002US-0365049P.
PR 22-MAR-2002; 2002US-0366802P.
PR 17-MAY-2002; 2002US-0381666P.
PR 18-JUN-2002; 2002US-0389531P.
PR 19-JUN-2002; 2002US-0389101P.
PR 25-JUN-2002; 2002US-0391516P.
PR 02-JUL-2002; 2002US-0393265P.
PR 07-AUG-2002; 2002US-0401825P.
PR 09-AUG-2002; 2002US-0402395P.
PR 12-AUG-2002; 2002US-0402867P.
PR 23-AUG-2002; 2002US-0405401P.
PR 23-AUG-2002; 2002US-0405820P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bader JS, Berghs C, Burgess CE, Casman SJ;
PI Catterton E, Chaudhuri A, Edinger SR, Ellerman K, Gerlach VL;
PI Gorman L, Guo X, Herrmann JL, Ji W, Khrantsov NV, Li L, Miller CE;
PI Ort T, Patturajan M, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
PI Spytek KA, Vernet CAM, Zhong H, Zhong M;
XX
WPI; 2003-646149/61.
DR N-PSDB; ADM29353.
XX
PT New NOVX polypeptide, useful for the manufacture of a medicament for
PT treating e.g., cancer or immune associated disorders.
XX
PS Claim 1; SEQ ID NO 98; 606pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC human proteins (NOV proteins). The DNA and protein sequences of the
CC invention are useful for the manufacture of a medicament for treating a
CC syndrome associated with a human disease comprising a pathology

CC associated with the protein, such as: cancer or immune associated
 CC disorders. The present amino acid sequence represents a NOV protein of
 CC the invention.

XX SQ Sequence 402 AA;

Query Match 97.0%; Score 128; DB 7; Length 402;
 Best Local Similarity 95.8%; Pred. NO. 7e-11;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLHNOEVTAEADGTQRAEKCKPCA 24
 Db 316 PLHNOEVTAEADGTQRAEKCKPCA 339

RESULT 6
 AAE09203
 ID AAE09203 standard; protein; 419 AA.

XX AAE09203;

XX 15 NOV-2001 (first entry)

DE Human p68HER-2 generic protein variant 1.

XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
 KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
 KW ECDIIIA; variant.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..340

FT /note= "Identical to N-terminal region of p185HER-2"

FT /notes "Represented as Agn in the parent sequence shown
 FT in the specification"

FT Misc-difference 125

FT /notes "Represented as Agn in the parent sequence shown
 FT in the specification"

FT Domain 341..419

FT /label= ECDIIIA variant

FT /notes "Extracellular domain IIIa variant"

FT Misc-difference 342

FT /notes "p68HER-2 generic sequence (AAE09181) Xaa
 FT substituted with Ser"

FT Misc-difference 345

FT /label= Unknown

FT Misc-difference 346

FT /label= Unknown

FT Misc-difference 356

FT /label= Unknown

FT Misc-difference 358

FT /label= Unknown

FT Misc-difference 361

FT /label= Unknown

FT Misc-difference 376

FT /label= Unknown

FT Misc-difference 394

FT /label= Unknown

FT Misc-difference 404

FT /label= Unknown

FT Misc-difference 413

FT /label= Unknown

XX WO200161356-A1.

XX 23-AUG-2001.

XX 16-FEB-2001; 2001WO-US005327.

XX 16-FEB-2000; 2000US-00506079.

XX

PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX Clinton G, Henner WD, Evans A;
 XX WPI; 2001-529934/58.

XX New polypeptide, which binds to the extracellular domain of HER-2 for the
 treatment of hard tumors.

XX Example 11; Page; 61pp; English.

CC The invention relates to novel HER-2 (herstatin-2) antagonist
 particularly a polypeptide that binds to the extracellular domain (ECD)
 of HER-2 at a site that is different from the binding site of humanised
 antibody, Herceptin, at an affinity of at least 10⁸. The present
 invention is based upon the initial discovery of an alternative HER-2
 mRNA transcript with 274 bp insert of intron 8. The translation product
 of the alternative transcript is a truncated HER-2 protein designated
 p68HER-2 which lacks the transmembrane and intracellular domains of
 p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
 The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
 the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
 nucleic acids encoding these are useful to treat, diagnose and identify
 solid tumours. The present sequence is human p68HER-2 generic protein
 containing ECDIIIA variant sequence. Note: The present sequence is not
 shown in the specification but is derived from p68HER-2 generic sequence
 (SEQ ID NO:2) shown in the sequence listing (AAE09181)

XX SQ Sequence 419 AA;

Query Match 97.0%; Score 128; DB 4; Length 419;
 Best Local Similarity 95.8%; Pred. NO. 7.4e-11;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 PLHNOEVTAEADGTQRAEKCKPCA 24

Db 316 PLHNOEVTAEADGTQRAEKCKPCA 339

RESULT 7

AAE09211

ID AAE09211 standard; protein; 419 AA.

XX AAE09211;

XX 15-NOV-2001 (first entry)

DE Human p68HER-2 generic protein variant 9.

XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
 KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
 KW ECDIIIA; variant.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..340

FT /note= "Identical to N-terminal region of p185HER-2"

FT Misc-difference 124

FT /note= "Represented as Agn in the parent sequence shown
 FT in the specification"

FT Misc-difference 125

FT /note= "Represented as Agn in the parent sequence shown
 FT in the specification"

FT Domain 341..419

FT /label= ECDIIIA variant

FT /note= "Extracellular domain IIIa variant"

FT Misc-difference 342

FT /label= Unknown

FT Misc-difference 345

FT /label= Unknown

FT Misc-difference 346

FT /label= Unknown

FT Misc-difference 356 /label= Unknown
 FT Misc-difference 358 /label= Unknown
 FT Misc-difference 361 /label= Unknown
 FT Misc-difference 376 /label= Unknown
 FT Misc-difference 394 /label= Unknown
 FT Misc-difference 404 /label= Unknown
 FT /note= "p68HER-2 generic sequence (AAE09181) Xaa
 substituted with Leu"
 FT Misc-difference 413 /label= Unknown
 FT W0200161356-A1.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005327.
 XX 16-FEB-2000; 2000US-00506079.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 XX Clinton G, Henner WD, Evans A;
 XX WPI; 2001-529934/58.
 XX New polypeptide, which binds to the extracellular domain of HER-2 for the
 treatment of hard tumors.
 XX Example 11; Page; 61pp; English.
 XX The invention relates to novel HER-2 (herstatin-2) antagonist
 particularly a polypeptide that binds to the extracellular domain (ECD)
 of HER-2 at a site that is different from the binding site of humanised
 antibody, Herceptin, at an affinity of at least 10⁸. The present
 invention is based upon the initial discovery of an alternative HER-2
 mRNA transcript with 274 bp insert of intron 8. The translation product
 of the alternative transcript is a truncated HER-2 protein designated
 p68HER-2 which lacks the transmembrane and intracellular domains of
 p185HER-2 but contains ECD 1, II of the p185HER-2 and the novel ECDIIIA.
 The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
 the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
 nucleic acids encoding these are useful to treat, diagnose and identify
 solid tumours. The present sequence is human p68HER-2 generic protein
 shown in the specification but is derived from p68HER-2 generic sequence
 (SEQ ID NO:2) shown in the sequence listing (AAE09181)
 XX Sequence 419 AA;
 Query Match 97.0%; Score 128; DB 4; Length 419;
 Best Local Similarity 95.8%; Pred. No. 7.4e-11;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 PLHNQVTAEDGTQRAEKCCKPCA 24
 Db 316 PLHNQVTAEDGTQRAEKCCKPCA 339
 RESULT 8
 ID AAE09210
 XX AAE09210 standard; protein; 419 AA.
 XX AAE09210;
 XX 15-NOV-2001 (first entry)
 XX Human p68HER-2 generic protein variant 8.
 DE Human p68HER-2 generic protein variant 8.
 XX

KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
 KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
 KW ECDIIIA; variant.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Region 1..340
 FT /note= "Identical to N-terminal region of p185HER-2"
 FT Misc-difference 124
 FT /note= "Represented as Agn in the parent sequence shown
 in the specification"
 FT Misc-difference 125
 FT /note= "Represented as Agn in the parent sequence shown
 in the specification"
 FT Domain 341..419
 FT /label= ECDIIIA_variant
 FT /note= "Extracellular domain IIIA variant"
 FT Misc-difference 342 /label= Unknown
 FT Misc-difference 345 /label= Unknown
 FT Misc-difference 346 /label= Unknown
 FT Misc-difference 356 /label= Unknown
 FT Misc-difference 358 /label= Unknown
 FT Misc-difference 361 /label= Unknown
 FT Misc-difference 376 /label= Unknown
 FT Misc-difference 394 /label= Unknown
 FT /note= "p68HER-2 generic sequence (AAE09181) Xaa
 substituted with Arg"
 FT Misc-difference 404 /label= Unknown
 FT Misc-difference 413 /label= Unknown
 FT W0200161356-A1.
 XX 23-AUG-2001.
 XX 16-FEB-2001; 2001WO-US005327.
 XX 16-FEB-2000; 2000US-00506079.
 XX (UYOR-) UNIV OREGON HEALTH SCI.
 XX Clinton G, Henner WD, Evans A;
 XX WPI; 2001-529934/58.
 XX New polypeptide, which binds to the extracellular domain of HER-2 for the
 treatment of hard tumors.
 XX Example 11; Page; 61pp; English.
 XX The invention relates to novel HER-2 (herstatin-2) antagonist
 particularly a polypeptide that binds to the extracellular domain (ECD)
 of HER-2 at a site that is different from the binding site of humanised
 antibody, Herceptin, at an affinity of at least 10⁸. The present
 invention is based upon the initial discovery of an alternative HER-2
 mRNA transcript with 274 bp insert of intron 8. The translation product
 of the alternative transcript is a truncated HER-2 protein designated
 p68HER-2 which lacks the transmembrane and intracellular domains of
 p185HER-2 but contains ECD 1, II of the p185HER-2 and the novel ECDIIIA.
 The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
 the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
 nucleic acids encoding these are useful to treat, diagnose and identify
 solid tumours. The present sequence is human p68HER-2 generic protein
 shown in the specification but is derived from p68HER-2 generic sequence
 (SEQ ID NO:2) shown in the sequence listing (AAE09181)
 XX Sequence 419 AA;
 Query Match 97.0%; Score 128; DB 4; Length 419;
 Best Local Similarity 95.8%; Pred. No. 7.4e-11;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 PLHNQVTAEDGTQRAEKCCKPCA 24
 Db 316 PLHNQVTAEDGTQRAEKCCKPCA 339
 RESULT 8
 ID AAE09210
 XX AAE09210 standard; protein; 419 AA.
 XX AAE09210;
 XX 15-NOV-2001 (first entry)
 XX Human p68HER-2 generic protein variant 8.
 DE Human p68HER-2 generic protein variant 8.
 XX

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CC shown in the specification but is derived from p68HER-2 generic sequence
CC (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ Sequence 419 AA;
Query Match 97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNOEVTAEEDGTORAEKCKPCA 24
Db 316 PLHNOEVTAEEDGTORCEKCKPCA 339
RESULT 9
AAE09205
ID AAE09205 standard; protein; 419 AA.
AC AAE09205;
XX
XX 15-NOV-2001 (first entry)
XX Human p68HER-2 generic protein variant 3.
XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
KW ECDIIIA; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..340
FT /note= "Identical to N-terminal region of p185HER-2"
FT Misc-difference 124
FT /note= "Represented as Agn in the parent sequence shown
FT in the specification"
FT Misc-difference 125
FT /note= "Represented as Agn in the parent sequence shown
FT in the specification"
FT Domain 341..419
FT /label= ECDIIIA variant
FT /note= "Extracellular domain IIIa variant"
FT Misc-difference 342
FT /label= Unknown
FT Misc-difference 345
FT /label= Unknown
FT Misc-difference 346
FT /label= Unknown
FT /note= "p68HER-2 generic sequence (AAE09181) Xaa
FT substituted with Leu"
FT Misc-difference 356
FT /label= Unknown
FT Misc-difference 358
FT /label= Unknown
FT Misc-difference 361
FT /label= Unknown
FT Misc-difference 376
FT /label= Unknown
FT Misc-difference 394
FT /label= Unknown
FT Misc-difference 404
FT /label= Unknown
FT Misc-difference 413
FT /label= Unknown
XX WO200161356-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX
XX 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
, PA
XX Clinton G, Henner WD, Evans A;
XX WPI; 2001-529934/58.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Example 11; Page; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIIA variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ Sequence 419 AA;
Query Match 97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNOEVTAEEDGTORAEKCKPCA 24
Db 316 PLHNOEVTAEEDGTORCEKCKPCA 339
RESULT 10
AAE09208
ID AAE09208 standard; protein; 419 AA.
XX
XX AAE09208;
XX
XX 15-NOV-2001 (first entry)
XX
XX Human p68HER-2 generic protein variant 6.
XX
XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
KW ECDIIIA; variant.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..340
FT /note= "Identical to N-terminal region of p185HER-2"
FT Misc-difference 124
FT /note= "Represented as Agn in the parent sequence shown
FT in the specification"
FT Misc-difference 125
FT /note= "Represented as Agn in the parent sequence shown
FT in the specification"
FT Domain 341..419
FT /label= ECDIIIA variant
FT /note= "Extracellular domain IIIa variant"
FT Misc-difference 342
FT /label= Unknown
FT Misc-difference 345
FT /label= Unknown
FT Misc-difference 346
FT /label= Unknown
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FT      /label= Unknown
FT      Misc-difference 358
FT      /label= Unknown
FT      Misc-difference 361
FT      /label= Asp, Ala, Val
FT      Misc-difference 376
FT      /label= Unknown
FT      Misc-difference 394
FT      /label= Unknown
FT      Misc-difference 404
FT      /label= Unknown
FT      Misc-difference 413
FT      /label= Unknown
FT      WO200161356-A1.
XX      XX
XX      23-AUG-2001.
XX      16-FEB-2001; 2001WO-US005327.
XX      16-FEB-2000; 2000US-00506079.
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX      Clinton G, Henner WD, Evans A;
XX      WPI; 2001-529934/58.
XX      New polypeptide, which binds to the extracellular domain of HER-2 for the
XX      treatment of hard tumors.
XX      Example 11; Page; 61pp; English.
XX      The invention relates to novel HER-2 (herstatin-2) antagonist
XX      particularly a polypeptide that binds to the extracellular domain (ECD)
XX      of HER-2 at a site that is different from the binding site of humanised
XX      antibody, Herceptin, at an affinity of at least 108. The present
XX      invention is based upon the initial discovery of an alternative HER-2
XX      mRNA transcript with 274 bp insert of intron 8. The translation product
XX      of the alternative transcript is a truncated HER-2 protein designated
XX      p68HER-2 which lacks the transmembrane and intracellular domains of
XX      p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX      The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX      the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX      nucleic acids encoding these are useful to treat, diagnose and identify
XX      solid tumours. The present sequence is human p68HER-2 generic protein
XX      containing ECDIIIA variant sequence. Note: The present sequence is not
XX      shown in the specification but is derived from p68HER-2 generic sequence
XX      (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX      Sequence 419 AA;
XX
XX      Query Match      97.0%; Score 128; DB 4; Length 419;
XX      Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY      1 PLHNQEVTAEDGTQRAEKCCKPCA 24
DB      316 PLHNQEVTAEDGTQRCCKPCA 339
XX
RESULT 11
AAE09206
ID      AAE09206 standard; protein; 419 AA.
XX      AAE09206;
XX      15-NOV-2001 (first entry)
XX      Human p68HER-2 generic protein variant 4.
XX      HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
XX      solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

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KW      ECDIIIA; variant.
XX      XX
XX      Homo sapiens.
XX      XX
XX      Key      Location/Qualifiers
XX      Region      1..340
XX      /note= "Identical to N-terminal region of p185HER-2"
XX      Misc-difference 124
XX      /note= "Represented as Agn in the parent sequence shown
XX      in the specification"
XX      Misc-difference 125
XX      /note= "Represented as Agn in the parent sequence shown
XX      in the specification"
XX      Domain      341..419
XX      /label= ECDIIIA variant
XX      /note= "Extracellular domain IIIa variant"
XX      Misc-difference 342
XX      /label= Unknown
XX      Misc-difference 345
XX      /label= Unknown
XX      Misc-difference 346
XX      /label= Unknown
XX      Misc-difference 356
XX      /note= "p68HER-2 generic sequence (AAE09181) Xaa
XX      substituted with Gln"
XX      Misc-difference 358
XX      /label= Unknown
XX      Misc-difference 361
XX      /label= Unknown
XX      Misc-difference 376
XX      /label= Unknown
XX      Misc-difference 394
XX      /label= Unknown
XX      Misc-difference 404
XX      /label= Unknown
XX      Misc-difference 413
XX      /label= Unknown
XX      WO200161356-A1.
XX      23-AUG-2001.
XX      16-FEB-2001; 2001WO-US005327.
XX      16-FEB-2000; 2000US-00506079.
XX      (UYOR-) UNIV OREGON HEALTH SCI.
XX      Clinton G, Henner WD, Evans A;
XX      WPI; 2001-529934/58.
XX      New polypeptide, which binds to the extracellular domain of HER-2 for the
XX      treatment of hard tumors.
XX      Example 11; Page; 61pp; English.
XX      The invention relates to novel HER-2 (herstatin-2) antagonist
XX      particularly a polypeptide that binds to the extracellular domain (ECD)
XX      of HER-2 at a site that is different from the binding site of humanised
XX      antibody, Herceptin, at an affinity of at least 108. The present
XX      invention is based upon the initial discovery of an alternative HER-2
XX      mRNA transcript with 274 bp insert of intron 8. The translation product
XX      of the alternative transcript is a truncated HER-2 protein designated
XX      p68HER-2 which lacks the transmembrane and intracellular domains of
XX      p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX      The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX      the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX      nucleic acids encoding these are useful to treat, diagnose and identify
XX      solid tumours. The present sequence is human p68HER-2 generic protein
XX      containing ECDIIIA variant sequence. Note: The present sequence is not
XX      shown in the specification but is derived from p68HER-2 generic sequence
XX      (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX      Sequence 419 AA;
XX
XX      Query Match      97.0%; Score 128; DB 4; Length 419;
XX      Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY      1 PLHNQEVTAEDGTQRAEKCCKPCA 24
DB      316 PLHNQEVTAEDGTQRCCKPCA 339
XX
RESULT 11
AAE09206
ID      AAE09206 standard; protein; 419 AA.
XX      AAE09206;
XX      15-NOV-2001 (first entry)
XX      Human p68HER-2 generic protein variant 4.
XX      HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
XX      solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

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FT Misc-difference 358 /label= Unknown
FT Misc-difference 361 /label= Unknown
FT Misc-difference 376 /label= Unknown
FT Misc-difference 394 /label= Unknown
FT Misc-difference 404 /label= Unknown
FT Misc-difference 413 /label= Unknown
FT /note= "p68HER-2 generic sequence (AAE09181) Xaa
FT substituted with Asn"
XX
XX WO200161356-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX
XX 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton G, Henner WD, Evans A;
XX
XX WPI; 2001-529934/58.
XX
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XX treatment of hard tumors.
XX
XX Example 11; Page; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD 1, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIIA variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
XX Sequence 419 AA;
XX
XX Query Match 97.0%; Score 128; DB 4; Length 419;
XX Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 PLHNQEVTAEDGTORAEKSKPCA 24
XX
XX Db 316 PLHNQEVTAEDGTORCEKSKPCA 339
XX
XX
XX RESULT 14
XX AAE09202
XX ID AAE09202 standard; protein; 419 AA.
XX
XX AC AAE09202;
XX
XX XX 15-NOV-2001 (first entry)
XX
XX DE Human p68HER-2 generic protein variant (Arg371Ile).
XX
XX KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
XX solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

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KW ECDIIIA; variant.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX XX 1. 340
XX Region
XX FT /note= "Identical to N-terminal region of p185HER-2"
XX FT Misc-difference 124
XX FT /note= "Represented as Agn in the parent sequence shown
XX FT in the specification"
XX FT Misc-difference 125
XX FT /note= "Represented as Agn in the parent sequence shown
XX FT in the specification"
XX FT Domain 341..419
XX FT /label= ECDIIIA variant
XX FT /note= "Extracellular domain IIIA variant"
XX
XX FT Misc-difference 342 /label= Unknown
XX FT Misc-difference 345 /label= Unknown
XX FT Misc-difference 346 /label= Unknown
XX FT Misc-difference 356 /label= Unknown
XX FT Misc-difference 358 /label= Unknown
XX FT Misc-difference 361 /label= Unknown
XX FT Misc-difference 371 /label= Unknown
XX FT /note= "p68HER-2 generic sequence (AAE09181) Arg
XX substituted with Ile"
XX FT Misc-difference 376 /label= Unknown
XX FT Misc-difference 394 /label= Unknown
XX FT Misc-difference 404 /label= Unknown
XX FT Misc-difference 413 /label= Unknown
XX
XX WO200161356-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX
XX 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton G, Henner WD, Evans A;
XX
XX WPI; 2001-529934/58.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Example 12; Page; 61pp; English.
XX
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XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD 1, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIIA variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
XX Sequence 419 AA;
XX
XX Query Match 97.0%; Score 128; DB 4; Length 419;
XX Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX Qy 1 PLHNQEVTAEDGTORAEKSKPCA 24
XX
XX Db 316 PLHNQEVTAEDGTORCEKSKPCA 339
XX
XX
XX RESULT 14
XX AAE09202
XX ID AAE09202 standard; protein; 419 AA.
XX
XX AC AAE09202;
XX
XX XX 15-NOV-2001 (first entry)
XX
XX DE Human p68HER-2 generic protein variant (Arg371Ile).
XX
XX KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
XX solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

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CC shown in the specification but is derived from p68HER-2 generic sequence
CC (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ Sequence 419 AA;

Query Match 97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQRCCKPCA 339

RESULT 15
AAE09214
ID AAE09214 standard; protein; 419 AA.
XX
AC AAE09214;
DT 15-NOV-2001 (first entry)
XX
DE Human p68HER-2 generic protein variant 13.
XX
KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
KW ECDIIIA; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..340
FT Misc-difference 124 /note= "Identical to N-terminal region of p185HER-2"
FT Misc-difference 125 /note= "Represented as Agn in the sequence shown in the
specification"
FT Domain 341..419
FT Misc-difference 342 /label= "ECDIIIA variant"
FT Misc-difference 343 /note= "Extracellular domain IIIa"
FT Misc-difference 344 /label= Unknown
FT Misc-difference 345 /label= Unknown
FT Misc-difference 346 /label= Unknown
FT Misc-difference 356 /label= Unknown
FT Misc-difference 357 /label= Unknown
FT Misc-difference 358 /note= "p68HER-2 generic sequence (AAE09183) Xaa
substituted with Cys"
FT Misc-difference 359 /label= Unknown
FT Misc-difference 361 /label= Unknown
FT Misc-difference 371 /label= Unknown
FT Misc-difference 376 /label= Unknown
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FT Misc-difference 404 /label= Unknown
FT Misc-difference 413 /label= Unknown
FT Misc-difference 419 /label= Unknown
XX
PN WO200161356-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005327.
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XX
PR 16-FEB-2000; 2000US-00506079.
XX
PA (UYOR-) UNIV OREGON HEALTH SCI.
XX
PI Clinton G, Henner WD, Evans A;
XX
DR WPI; 2001-529934/58.
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treatment of hard tumors.
XX
PS Example 12; Page; 61pp; English.
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CC particularly a polypeptide that binds to the extracellular domain (ECD)
CC of HER-2 at a site that is different from the binding site of humanised
CC antibody, Herceptin, at an affinity of at least 108. The present
CC invention is based upon the initial discovery of an alternative HER-2
CC mRNA transcript with 274 bp insert of intron 8. The translation product
CC of the alternative transcript is a truncated HER-2 protein designated
CC p68HER-2 which lacks the transmembrane and intracellular domains of
CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
CC nucleic acids encoding these are useful to treat, diagnose and identify
CC solid tumours. The present sequence is human p68HER-2 generic protein
CC containing ECDIIIA variant sequence. Note: The present sequence is not
CC shown in the specification but is derived from p68HER-2 generic sequence
CC (SEQ ID NO:13) shown in the sequence listing (AAE09183)
XX
SQ Sequence 419 AA;

Query Match 97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQRCCKPCA 339

RESULT 16
AAE09212
ID AAE09212 standard; protein; 419 AA.
XX
AC AAE09212;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human p68HER-2 generic protein variant 10.
XX
KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
KW ECDIIIA; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..340
FT Misc-difference 124 /note= "Identical to N-terminal region of p185HER-2"
FT Misc-difference 125 /note= "Represented as Agn in the parent sequence shown
in the specification"
FT Domain 341..419
FT Misc-difference 342 /label= "Extracellular domain IIIa variant"
FT Misc-difference 343 /label= Unknown
FT Misc-difference 345
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FT Misc-difference 346 /label= Unknown
FT Misc-difference 356 /label= Unknown
FT Misc-difference 356 /label= Unknown
FT Misc-difference 358 /label= Unknown
FT Misc-difference 361 /label= Unknown
FT Misc-difference 376 /label= Unknown
FT Misc-difference 394 /label= Unknown
FT Misc-difference 404 /label= Unknown
FT Misc-difference 413 /label= Unknown
FT /note= "p68HER-2 generic sequence (AAE09181) Xaa
FT substituted with Asn"
XX
PN WO200161356-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX
XX 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton G, Henner WD, Evans A;
XX
XX WPI; 2001-529934/58.
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XX treatment of hard tumors.
XX
XX Example 11; Page; 61pp; English.
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XX of HER-2 at a site that is different from the binding site of humanised
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XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIa.
XX The ECDIIa-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIa variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ Sequence 419 AA;

Query Match 97.08; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTORAEKSKPCA 24
Db 316 PLHNQEVTAEDGTORCEKSKPCA 339
|||||

RESULT 17
AAE09215
ID AAE09215 standard; protein; 419 AA.
XX
XX AAE09215;
AC
XX
XX 15-NOV-2001 (first entry)

XX Human p68HER-2 generic protein variant 14.
DE
XX
XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
KW ECDIIa; variant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Region 1..340
FT /note= "Identical to N-terminal region of p185HER-2"
FT Misc-difference 124
FT /note= "Represented as Agn in the sequence shown in the
FT specification"
FT Misc-difference 125
FT /note= "Represented as Agn in the sequence shown in the
FT specification"
FT Domain 341..419
FT /label= ECDIIa variant
FT /note= "Extracellular domain IIIa"
FT Misc-difference 342 /label= Unknown
FT Misc-difference 345 /label= Unknown
FT Misc-difference 346 /label= Unknown
FT Misc-difference 356 /label= Unknown
FT Misc-difference 357 /label= Unknown
FT Misc-difference 358 /label= Unknown
FT Misc-difference 361 /label= Unknown
FT Misc-difference 371 /label= Unknown
FT /note= "p68HER-2 generic sequence (AAE09183) Xaa
FT substituted with Ile"
FT Misc-difference 376 /label= Unknown
FT Misc-difference 394 /label= Unknown
FT Misc-difference 404 /label= Unknown
FT Misc-difference 413 /label= Unknown
XX WO200161356-A1.
PN 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX
XX 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton G, Henner WD, Evans A;
XX WPI; 2001-529934/58.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Example 12; Page; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 10⁸. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIa.
XX The ECDIIa-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIa variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ Sequence 419 AA;

Query Match 97.08; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTORAEKSKPCA 24
Db 316 PLHNQEVTAEDGTORCEKSKPCA 339
|||||

RESULT 17
AAE09215
ID AAE09215 standard; protein; 419 AA.
XX
XX AAE09215;
AC
XX
XX 15-NOV-2001 (first entry)

CC p68HER-2 which lacks the transmembrane and intracellular domains of
 CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
 CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
 CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
 CC nucleic acids encoding these are useful to treat, diagnose and identify
 CC solid tumours. The present sequence is human p68HER-2 generic protein
 CC containing ECDIIIA variant sequence. Note: The present sequence is not
 CC shown in the specification but is derived from p68HER-2 generic sequence
 CC (SEQ ID NO:13) shown in the sequence listing (AAE09183)
 XX
 SQ Sequence 419 AA;
 Query Match 97.0%; Score 128; DB 4; Length 419;
 Best Local Similarity 95.8%; Pred. No. 7.4e-11;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 , : F:LNQEVTAEDGTQRAEKCCKPCA 24
 Db 316 PLHNQEVTAEDGTQRCCKCKPCA 339
 RESULT 18
 AAE09216
 ID AAE09216 standard; protein; 419 AA.
 XX
 AC AAE09216;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Human p68HER-2 generic protein variant 15.
 XX
 KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
 KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
 KW ECDIIIA; variant.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..340
 FT /note= "Identical to N-terminal region of p185HER-2"
 FT Misc-difference 124
 FT /note= "Represented as Agn in the sequence shown in the
 FT specification"
 FT Misc-difference 125
 FT /note= "Represented as Agn in the sequence shown in the
 FT specification"
 FT Domain 341..419
 FT /label= ECDIIIA variant
 FT /note= "Extracellular domain IIIa"
 FT Misc-difference 342
 FT /label= Unknown
 FT Misc-difference 345
 FT /label= Unknown
 FT Misc-difference 346
 FT /label= Unknown
 FT Misc-difference 356
 FT /label= Unknown
 FT Misc-difference 357
 FT /label= Unknown
 FT Misc-difference 358
 FT /label= Unknown
 FT Misc-difference 361
 FT /label= Unknown
 FT Misc-difference 371
 FT /label= Unknown
 FT Misc-difference 376
 FT /label= Unknown
 FT Misc-difference 394
 FT /label= Unknown
 FT Misc-difference 404
 FT /label= Unknown
 FT Misc-difference 413
 FT /note= "p68HER-2 generic sequence (AAE09183) Xaa
 FT

FT substituted with Asn"
 XX WO200161356-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-US005327.
 XX
 PR 16-FEB-2000; 2000US-00506079.
 XX
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX
 PI Clinton G, Henner WD, Evans A;
 XX WPI; 2001-529934/58.
 XX
 PT New polypeptide, which binds to the extracellular domain of HER-2 for the
 FT treatment of hard tumors.
 XX
 PS Example 12; Page; 61pp; English.
 XX
 CC The invention relates to novel HER-2 (herstatin-2) antagonist
 CC particularly a polypeptide that binds to the extracellular domain (ECD)
 CC of HER-2 at a site that is different from the binding site of humanised
 CC antibody, Herceptin, at an affinity of at least 10⁸. The present
 CC invention is based upon the initial discovery of an alternative HER-2
 CC mRNA transcript with 274 bp insert of intron 8. The translation product
 CC of the alternative transcript is a truncated HER-2 protein designated
 CC p68HER-2 which lacks the transmembrane and intracellular domains of
 CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
 CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
 CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
 CC nucleic acids encoding these are useful to treat, diagnose and identify
 CC solid tumours. The present sequence is human p68HER-2 generic protein
 CC containing ECDIIIA variant sequence. Note: The present sequence is not
 CC shown in the specification but is derived from p68HER-2 generic sequence
 CC (SEQ ID NO:13) shown in the sequence listing (AAE09183)
 XX
 SQ Sequence 419 AA;
 Query Match 97.0%; Score 128; DB 4; Length 419;
 Best Local Similarity 95.8%; Pred. No. 7.4e-11;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
 Db 316 PLHNQEVTAEDGTQRCCKCKPCA 339
 RESULT 19
 AAE09181
 ID AAE09181 standard; protein; 419 AA.
 XX
 AC AAE09181;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Human p68HER-2 generic sequence #1.
 XX
 KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
 KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
 KW ECDIIIA.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..340
 FT /note= "Identical to N-terminal region of p185HER-2"
 FT Misc-difference 124
 FT /note= "Represented as Agn in the sequence shown in the
 FT specification"
 FT Misc-difference 125
 FT /note= "Represented as Agn in the sequence shown in the
 FT specification"
 FT


```

FT Misc-difference 413
FT FT /label= Unknown
FT FT /note= "Encoded by VAC"
XX PN
XX
XX WO200161356-A1.
XX
XX 23-AUG-2001.
XX
XX 16-FEB-2001; 2001WO-US005327.
XX PF
XX 16-FEB-2000; 2000US-00506079.
XX PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX PA
XX Clinton G, Henner WD, Evans A;
XX PI
XX WPI; 2001-529934/58.
XX DR
XX N-PSDB; AADI5852.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Claim 8; Page 57-58; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 protein containing
XX ECDIIIA generic sequence
XX
XX Sequence 419 AA;
XX
XX Query Match 97.0%; Score 128; DB 4; Length 419;
XX Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
DB 316 PLHNQEVTAEDGTQRAEKCKPCA 339
|||||
|||||

RESULT 21
AAE09200
ID AAE09200 standard; protein; 419 AA.
XX AC
XX AAE09200;
XX
XX 15-NOV-2001 (first entry)
XX
XX Human p68HER-2 generic protein variant (Arg357Cys).
XX
XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;
XX solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;
XX ECDIIIA; variant.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 1..340
XX /note= "Identical to N-terminal region of p185HER-2"
XX FT Misc-difference 124
XX /note= "Represented as Agn in the parent sequence shown
XX in the specification"
XX FT Misc-difference 125

```

```

FT FT /note= "Represented as Agn in the parent sequence shown
FT in the specification"
FT 341..419
FT /label= ECDIIIA variant
FT /note= "Extracellular domain IIIa variant"
FT Misc-difference 342
FT /label= Unknown
FT Misc-difference 345
FT /label= Unknown
FT Misc-difference 346
FT /label= Unknown
FT Misc-difference 356
FT /label= Unknown
FT Misc-difference 357
FT /note= "p68HER-2 generic sequence (AAE09181) Arg
FT substituted with Cys"
FT Misc-difference 358
FT /label= Unknown
FT Misc-difference 361
FT /label= Unknown
FT Misc-difference 376
FT /label= Unknown
FT Misc-difference 394
FT /label= Unknown
FT Misc-difference 404
FT /label= Unknown
FT Misc-difference 413
FT /label= Unknown
XX WO200161356-A1.
XX 23-AUG-2001.
XX 16-FEB-2001; 2001WO-US005327.
XX PF
XX 16-FEB-2000; 2000US-00506079.
XX PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX PA
XX Clinton G, Henner WD, Evans A;
XX PI
XX WPI; 2001-529934/58.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Example 12; Page; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic sequence
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
XX Sequence 419 AA;
XX
XX Query Match 97.0%; Score 128; DB 4; Length 419;
XX Best Local Similarity 95.8%; Pred. No. 7.4e-11;
XX Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
DB 316 PLHNQEVTAEDGTQRAEKCKPCA 339
|||||
|||||

Query Match 97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Db 316 PLHNOEVTABDGTORCEKCKSKPCA 339

RESULT 22

AAE09204

ID AAE09204 standard; protein; 419 AA.

AC AAE09204;

XX

DT 15-NOV-2001 (first entry)

XX

DE Human p68HER-2 generic protein variant 2.

XX

XX HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;

KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

KW ECDIIIA; variant.

XX

OS Homo sapiens.

XX

PH Key

FT Region 1. .340

FT Location/Qualifiers

FT /note= "Identical to N-terminal region of p185HER-2"

FT Misc-difference 124

FT /note= "Represented as Agn in the parent sequence shown

FT in the specification"

FT Misc-difference 125

FT /note= "Represented as Agn in the parent sequence shown

FT in the specification"

FT Domain 341..419

FT /label= ECDIIIA variant

FT /note= "Extracellular domain IIIa variant"

FT Misc-difference 342

FT /label= Unknown

FT Misc-difference 345

FT /note= "p68HER-2 generic sequence (AAE09181) Xaa

FT substituted with Pro"

FT Misc-difference 346

FT /label= Unknown

FT Misc-difference 356

FT /label= Unknown

FT Misc-difference 358

FT /label= Unknown

FT Misc-difference 361

FT /label= Unknown

FT Misc-difference 376

FT /label= Unknown

FT Misc-difference 394

FT /label= Unknown

FT Misc-difference 404

FT /label= Unknown

FT Misc-difference 413

FT /label= Unknown

XX WO200161356-A1.

PN

XX

PD 23-AUG-2001.

XX

PF 16-FEB-2001; 2001WO-US005327.

XX

PR 16-FEB-2000; 2000US-00506079.

XX

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX

XX Clinton G, Henner WD, Evans A;

PI

XX WPI; 2001-529934/58.

DR

XX

XX New polypeptide, which binds to the extracellular domain of HER-2 for the

PT treatment of hard tumors.

XX

XX Example 11; Page; 61pp; English.

PS

XX The invention relates to novel HER-2 (herstatin-2) antagonist

CC

CC particularly a polypeptide that binds to the extracellular domain (ECD)

CC of HER-2 at a site that is different from the binding site of humanised

CC antibody, Herceptin, at an affinity of at least 10⁸. The present

CC invention is based upon the initial discovery of an alternative HER-2

CC mRNA transcript with 274 bp insert of intron 8. The translation product

CC of the alternative transcript is a truncated HER-2 protein designated

CC p68HER-2 which lacks the transmembrane and intracellular domains of

CC p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.

CC The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise

CC the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the

CC nucleic acids encoding these are useful to treat, diagnose and identify

CC solid tumours. The present sequence is human p68HER-2 generic protein

CC containing ECDIIIA variant sequence. Note: The present sequence is not

CC shown in the specification but is derived from p68HER-2 generic sequence

CC (SEQ ID NO:2) shown in the sequence listing (AAE09181)

XX

SQ Sequence 419 AA;

Query Match 97.0%; Score 128; DB 4; Length 419;

Best Local Similarity 95.8%; Pred. No. 7.4e-11;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNOEVTABDGTORAEKCKSKPCA 24

Db 316 PLHNOEVTABDGTORCEKCKSKPCA 339

|||||||

|||||||

RESULT 23

AAE09209

ID AAE09209 standard; protein; 419 AA.

XX

AC AAE09209;

XX

DT 15-NOV-2001 (first entry)

XX

XX Human p68HER-2 generic protein variant 7.

DE

XX

KW HER-2; herstatin; antagonist; extracellular domain; ECD; Herceptin;

KW solid tumour; cancer; polymorphism; cytostatic; gene therapy; p68HER-2;

KW ECDIIIA; variant.

XX

OS Homo sapiens.

XX

PH Key

FT Region 1. .340

FT Location/Qualifiers

FT /note= "Identical to N-terminal region of p185HER-2"

FT Misc-difference 124

FT /note= "Represented as Agn in the parent sequence shown

FT in the specification"

FT Misc-difference 125

FT /note= "Represented as Agn in the parent sequence shown

FT in the specification"

FT Domain 341..419

FT /label= ECDIIIA variant

FT /note= "Extracellular domain IIIa variant"

FT Misc-difference 342

FT /label= Unknown

FT Misc-difference 345

FT /label= Unknown

FT Misc-difference 346

FT /label= Unknown

FT Misc-difference 356

FT /label= Unknown

FT Misc-difference 358

FT /label= Unknown

FT Misc-difference 361

FT /label= Unknown

FT Misc-difference 376

FT /label= Unknown

FT Misc-difference 394

FT /label= Unknown

FT Misc-difference 404

FT /label= Unknown

FT Misc-difference 413

FT /label= Unknown

XX WO200161356-A1.

PN

XX

PD 23-AUG-2001.

XX

PF 16-FEB-2001; 2001WO-US005327.

XX

PR 16-FEB-2000; 2000US-00506079.

XX

XX (UYOR-) UNIV OREGON HEALTH SCI.

XX

XX Clinton G, Henner WD, Evans A;

PI

XX WPI; 2001-529934/58.

DR

XX

XX New polypeptide, which binds to the extracellular domain of HER-2 for the

PT treatment of hard tumors.

XX

XX Example 11; Page; 61pp; English.

PS

XX The invention relates to novel HER-2 (herstatin-2) antagonist

CC

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FT      /label= Unknown
FT Misc-difference 413
FT      /label= Unknown
AX
PN WO200161356-A1.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-US005327.
XX
PR 16-FEB-2000; 2000US-00506079.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton G, Henner WD, Evans A;
XX WPI; 2001-529934/58.
XX
XX New polypeptide, which binds to the extracellular domain of HER-2 for the
XX treatment of hard tumors.
XX
XX Example 11; Page; 61pp; English.
XX
XX The invention relates to novel HER-2 (herstatin-2) antagonist
XX particularly a polypeptide that binds to the extracellular domain (ECD)
XX of HER-2 at a site that is different from the binding site of humanised
XX antibody, Herceptin, at an affinity of at least 108. The present
XX invention is based upon the initial discovery of an alternative HER-2
XX mRNA transcript with 274 bp insert of intron 8. The translation product
XX of the alternative transcript is a truncated HER-2 protein designated
XX p68HER-2 which lacks the transmembrane and intracellular domains of
XX p185HER-2 but contains ECD I, II of the p185HER-2 and the novel ECDIIIA.
XX The ECDIIIA-containing polypeptides bind tightly to, and thus antagonise
XX the HER-2 receptor. The peptides, which bind to an HER-2 ECD, and the
XX nucleic acids encoding these are useful to treat, diagnose and identify
XX solid tumours. The present sequence is human p68HER-2 generic protein
XX containing ECDIIIA variant sequence. Note: The present sequence is not
XX shown in the specification but is derived from p68HER-2 generic sequence
XX (SEQ ID NO:2) shown in the sequence listing (AAE09181)
XX
SQ      Sequence 419 AA;
      Query Match      97.0%; Score 128; DB 4; Length 419;
      Best Local Similarity 95.8%; Pred. No. 7.4e-11;
      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 PLHNOEVTAEDGTQRAEKCKPCA 24
      |||||
DB      316 PLHNOEVTAEDGTQRCCKPCA 339

RESULT 24
AAE20348
ID AAE20348 standard; protein; 419 AA.
XX
XX AAE20348;
AC
XX
XX 18-JUN-2002 (first entry)
DT
XX
XX Human truncated HER2 protein.
DE
XX
XX Human; tumour; endothelial growth factor receptor; EGFR; cytostatic;
KW herstatin; HER-2 receptor tyrosine kinase; squamous cell carcinoma; lung;
KW colon; glial cell tumour; cell growth.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 342
FT      /label= Thr, Ser
FT Misc-difference 345
FT      /label= Leu, Pro
FT Misc-difference 346

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```

FT      /label= Pro, Leu
FT Misc-difference 356
FT      /label= Leu, Gln
FT Misc-difference 358
FT      /label= Met, Leu
FT Misc-difference 361
FT      /label= Gly, Asp, Ala, Val
FT Misc-difference 376
FT      /label= Leu, Ile
FT Misc-difference 394
FT      /label= Pro, Arg
FT Misc-difference 404
FT      /label= Pro, Leu
FT Misc-difference 413
FT      /label= Asp, Asn
XX
XX WO200214470-A2.
XX
XX 21-FEB-2002.
XX
XX 14-AUG-2001; 2001WO-US025502.
XX
XX 14-AUG-2000; 2000US-00638834.
XX
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX
XX Clinton GM;
XX
XX WPI; 2002-269185/31.
XX
XX Treating solid tumor characterized by expression of endothelial growth
XX factor receptor, involves administering recombinant herstatin that binds
XX to extracellular domain of the endothelial growth factor receptor.
XX
XX Claim 1; Page 78-80; 82pp; English.
XX
XX The present invention relates to a method for treating a solid tumour
XX characterised by endothelial growth factor receptor (EGFR) expression.
XX The method involves administering an agent that binds to an extracellular
XX domain (ECD) of EGFR. The invention also relates to a naturally occurring
XX inhibitor of HER-2 receptor tyrosine kinase called herstatin. The co-
XX expression of herstatin with p185HER2 causes a striking reduction in cell
XX growth that corresponds with suppression of p185 autophosphorylation. The
XX method or a pharmaceutical composition is useful for treating a solid
XX tumour (selected from squamous cell carcinoma, lung carcinoma, colon
XX carcinoma and glial cell tumour) characterised by EGFR expression. The
XX present sequence is human truncated HER2 protein that lacks transmembrane
XX and intracellular domains
XX
SQ      Sequence 419 AA;
      Query Match      97.0%; Score 128; DB 5; Length 419;
      Best Local Similarity 95.8%; Pred. No. 7.4e-11;
      Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 PLHNOEVTAEDGTQRAEKCKPCA 24
      |||||
DB      316 PLHNOEVTAEDGTQRCCKPCA 339

RESULT 25
ADP16709
ID ADF16709 standard; protein; 419 AA.
XX
XX ADF16709;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Human albumin fusion protein-related protein Segid1811.
DE
XX
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.

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XX OS Homo sapiens.
XX PN WO2003060071-A2.
XX PD 24-JUL-2003.
XX PF 23-DEC-2002; 2002WO-US040891.
XX PR 21-DEC-2001; 2001US-0341811P.
XX PR 24-JAN-2002; 2002US-0350358P.
XX PR 28-JAN-2002; 2002US-0351360P.
XX PR 26-FEB-2002; 2002US-0359370P.
XX PR 28-FEB-2002; 2002US-0360000P.
XX PR 27-MAR-2002; 2002US-0367500P.
XX PR 08-APR-2002; 2002US-0370227P.
XX PR 10-MAY-2002; 2002US-0378950P.
XX PR 24-MAY-2002; 2002US-0382617P.
XX PR 28-MAY-2002; 2002US-0383123P.
XX PR 05-JUN-2002; 2002US-0385708P.
XX PR 10-JUL-2002; 2002US-0394625P.
XX PR 24-JUL-2002; 2002US-0398008P.
XX PR 09-AUG-2002; 2002US-0402131P.
XX PR 13-AUG-2002; 2002US-0402708P.
XX PR 18-SEP-2002; 2002US-0411355P.
XX PR 18-SEP-2002; 2002US-0411436P.
XX PR 02-OCT-2002; 2002US-0414984P.
XX PR 11-OCT-2002; 2002US-0417611P.
XX PR 23-OCT-2002; 2002US-0420246P.
XX PR 05-NOV-2002; 2002US-0423623P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA (DELZ) DELTA BIOTECHNOLOGY LTD.
XX PA (PRIN-) PRINCIPIA PHARM CORP.
XX PI Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
XX PT WPI; 2003-598517/56.
XX DR N-PSDB; ADF16383.
XX PT New albumin fusion protein, useful for preparing a composition for treating diabetes mellitus.
XX PS Example 4; SEQ ID NO 1811; 24pp; English.
XX CC This invention relates to a novel albumin fusion protein having albumin or biological activity. Human serum albumin is responsible for a significant proportion of the osmotic pressure of serum and also functions as a carrier of endogenous and exogenous ligands. The fusion of albumin to a therapeutic protein may increase shelf-life and stability of the therapeutic protein. The albumin fusion protein of the invention may allow production of compositions with antidiabetic activity whilst the nucleotide sequence which encodes it may be useful for gene therapy. The albumin fusion protein is useful for preparing a composition for treating diabetes mellitus. The present sequence is that of a therapeutic protein which was fused with human albumin to create a novel albumin fusion protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/publishedpct_sequences

Query Match 97.08; Score 128; DB 7; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
|||||
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 26
ADY28119

ID ADY28119 standard; protein; 419 AA.
XX AC ADY28119;
XX DT 05-MAY-2005 (first entry)
XX DE Receptor tyrosine kinase protein - SEQ ID 9.
XX KW receptor tyrosine kinase; angiogenesis; cell proliferation; cell migration; cell growth; metastasis; cancer; cytostatic; rheumatoid arthritis; antiarthritic; antineumatic; multiple sclerosis; neuroprotective; inflammation; antiinflammatory; uveitis; ophthalmological; ocular inflammation; atherosclerosis; antiarteriosclerotic; hemangioma; diabetes mellitus; inflammatory bowel disease; gastrointestinal-gen.; Crohns disease; psoriasis; antipsoriatic; Alzheimers disease; neuroprotective; nootropic; systemic lupus erythematosus; restenosis; vasotropic; asthma; antiasthmatic; receptor tyrosine kinase.
XX OS Unidentified.
XX PN WO2005016966-A2.
XX PD 24-FEB-2005.
XX PF 14-MAY-2004; 2004WO-US015056.
XX PR 16-MAY-2003; 2003US-0471141P.
XX PA (RECE-) RECEPTOR BIOLOGIX INC.
XX PA (JINP/) JIN P.
XX PI Jin P, Shepard HM, Clinton GM, Lackey DB;
XX DR WPI; 2005-182332/19.
XX PT New receptor tyrosine kinase isoforms (such as TEK (TIE-2)), useful for treating a disease or condition, e.g. cancers, or inflammatory, infectious, immune, or neurodegenerative diseases.
XX PS Example 1; SEQ ID NO 9; 105pp; English.
XX CC The invention comprises the amino acid sequence of a number of receptor tyrosine kinase proteins which are useful for identifying drugs that modulate the receptor and for inhibiting angiogenesis, cell proliferation, cell migration, tumor cell growth or tumor cell metastasis. The receptor tyrosine kinase proteins of the invention are useful for treating cancers, rheumatoid arthritis, multiple sclerosis and posterior intraocular inflammation, uveitic disorders, ocular surface inflammatory disorders, neovascular disease, proliferative vitreoretinopathy, atherosclerosis, hemangioma, diabetes mellitus, inflammatory bowel disease, Crohn's disease, psoriasis, Alzheimer's disease, lupus, vascular stenosis, restenosis, inflammatory joint disease, urinary obstructive syndromes, and asthma. The present amino acid sequence represents a receptor tyrosine kinase protein of the invention. NOTE: The present sequence is not shown in the specification, but has been retrieved from the WIPO website.

Query Match 97.0%; Score 128; DB 9; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
|||||
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 27
ADZ47861
ID ADZ47861 standard; protein; 419 AA.
XX

AC AD247861;
XX 30-JUN-2005 (first entry)
XX Wild-type human ErbB-2 protein.
XX epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic.
XX Homo sapiens.
XX WO2005033133-A2.
PN 14-APR-2005.
XX 04-OCT-2004; 2004WO-US030903.
XX 03-OCT-2003; 2003US-0507953P.
PR 10-NOV-2003; 2003US-0518321P.
PR 09-AUG-2004; 2004US-059583P.
PR 07-SEP-2004; 2004US-0607326P.
XX (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
XX Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX WPI; 2005-285403/29.
XX New isolated polynucleotide encoding at least an active portion of an
PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
PT aberrant expression or activity of the ErbB-2 polypeptides, such as
PT cancer.
XX Disclosure; Fig 4; 246pp; English.
XX The invention relates to the isolation of polynucleotide sequences
CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
CC treatment of ErbB-2 related cancer. The sequences, methods, and
CC compositions of the present invention are useful for diagnosing,
CC prognosing, and/or treating diseases or conditions associated with
CC aberrant expression or activity of the ErbB-2 polypeptides, such as
CC cancer. This sequence represents the wild-type human ErbB-2 protein.
XX
SQ Sequence 419 AA;
Query Match 97.0%; Score 128; DB 9; Length 419;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNOEVTAEDGTQRAEKCSPCA 24
|||||
Db 316 PLHNOEVTAEDGTQRAEKCSPCA 339
RESULT 28
AAY97240
ID AAY97240 standard; protein; 420 AA.
XX AAY97240;
AC AAY97240;
XX 04-DEC-2000 (first entry)
DT Truncated HER-2, p68-HER-2.
XX
DE HER-2; erbB-2; oncogene; receptor-like tyrosine kinase; insertion;
KW extracellular domain IIIa; antagonist; intron 8; C-terminal extension;
KW truncated HER-2; p68; dimerization inhibitor; cytostatic.
XX Homo sapiens.
OS

XX Key Location/Qualifiers
FH Misc-difference 124 /note= "represented as Agn"
FT Misc-difference 125 /note= "represented as Agn"
FT Misc-difference 343 /note= "Preferably Ser"
FT Misc-difference 346 /note= "Preferably Pro"
FT Misc-difference 347 /note= "Preferably Leu"
FT Misc-difference 357 /note= "Preferably Gln"
FT Misc-difference 359 /note= "Preferably Leu"
FT Misc-difference 362 /note= "changes from glycine"
FT Misc-difference 377 /note= "Preferably Ile"
FT Misc-difference 395 /note= "Preferably Arg"
FT Misc-difference 405 /note= "Preferably Leu"
FT Misc-difference 414 /note= "Preferably Asn"
XX WO200044403-A1.
XX 03-AUG-2000.
XX 20-JAN-2000; 2000WO-US001484.
XX 20-JAN-1999; 99US-00234208.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Doherty JK, Clinton GM, Adelman JP;
PI WPI; 2000-499287/44.
XX Using polypeptides and antibodies that bind to the extracellular domain
PT of the receptor-like tyrosine kinase HER-2 to treat solid tumors of the
PT breast, lung, ovaries and colon.
XX Claim 8; Page 39-40; 46pp; English.
XX HER-2/neu (erbB-2) oncogene encodes a receptor-like tyrosine kinase. The
CC extracellular domain of p185-HER-2 is proteolytically shed from breast
CC carcinoma cells in culture and is found in serum of some cancer patients
CC and may be a serum marker of metastatic breast cancer. An alternative HER
CC -2 mRNA of 4.8 kb with a 274 bp insert (intron 8) has been identified.
CC The retained intron is in-frame and encodes a 79 amino acid extension
CC designated ECDIIa (the present sequence), which is inserted at residue
CC 340 of p185-HER-2. The alternative mRNA predicts a truncated HER-2
CC protein (approximately 68 kDa) that lacks the transmembrane and
CC intracellular domains (see AAY97240). p68HER-2 specifically binds to p185
CC -HER-2 without activating HER-2. It could therefore block dimerization of
CC p185-HER-2. The p68HER-2 polypeptide binds to a site on the ECD of HER-2
CC that is different from the site of binding for Herceptin (RTM) (a
CC marketed humanized monoclonal antibody that is used for the treatment of
CC cancer and binds to the ECD of HER-2). The methods, compositions,
CC polypeptides and antibodies are used to treat solid tumours such as
CC breast cancer, small cell lung carcinoma, ovarian cancer and/or colon
CC cancer, especially where over-expression of HER-2 is indicated
XX
SQ Sequence 420 AA;
Query Match 97.0%; Score 128; DB 3; Length 420;
Best Local Similarity 95.8%; Pred. No. 7.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNOEVTAEDGTQRAEKCSPCA 24

```
Db      316 PLHNQEVTAEDGTQCEKCKPCA 339
|||||
RESULT 29
AAE36793
ID  AAE36793 standard; protein; 509 AA.
AC  AAE36793;
XX
XX  07-AUG-2003 (first entry)
XX
XX  Human ErbB-2 protein.
XX
XX  Epidermal growth factor receptor; EGFR; therapy; psoriasis; carcinoma;
XX  cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human;
XX  receptor; ErbB-2.
XX
XX  Homo sapiens.
XX
XX  WO2003014159-A1.
XX
XX  20-FEB-2003.
XX
XX  05 AUG 2002; 2002WO-AU001042.
XX
XX  03-AUG-2001; 2001AU-00006927.
XX
XX  03-AUG-2001; 2001AU-00006928.
XX
XX  01-NOV-2001; 2001US-0335333P.
XX
XX  01-NOV-2001; 2001US-0336560P.
XX
XX  31-MAY-2002; 2002AU-00002731.
XX
XX  11-JUN-2002; 2002US-0388171P.
XX
XX  (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX  (BIOM-) BIOMOLECULAR RES INST LTD.
XX  (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX  (LUDW-) LUDWIG INST CANCER RES.
XX
XX  Adams TE, Burgess AW, Elleman TC, Garrett TPJ, Jorissen RN;
XX  Lou M, Lovrecz GO, Mckern NM, Nice EC, Ward CW;
XX  WPI; 2003-268181/26.
XX
XX  Selecting or designing compounds that interact with or inhibit formation
XX  of active dimers of the EGF receptor family, and useful for the
XX  prevention and treatment of disorders, such as psoriasis and cancer of
XX  the breast, brain or colon.
XX
XX  Disclosure; Fig 1; 354pp; English.
XX
XX  The invention relates to a method of selecting or designing a compound
XX  that interacts with or inhibits the formation of active dimers of a
XX  receptor of the epidermal growth factor receptor (EGFR) family. The
XX  methods and compositions of the invention are useful for the prevention
XX  and treatment of disorders associated with signalling by a molecule of
XX  the EGFR family such as psoriasis and cancer of the pancreas, breast,
XX  brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma,
XX  rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and
XX  glioblastomas. The present sequence is human ErbB-2 protein. This
XX  sequence is used to illustrate the method of the invention
XX
XX  Sequence 509 AA;
Query Match      97.0%; Score 128; DB 6; Length 509;
Best Local Similarity 95.8%; Pred. No. 9.1e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 PLHNQEVTAEDGTQCEKCKPCA 24
        |||||||
Db      295 PLHNQEVTAEDGTQCEKCKPCA 318
|||||
RESULT 30
AAE36793
ID  AAE36793 standard; protein; 509 AA.
AC  AAE36793;
XX
XX  07-AUG-2003 (first entry)
XX
XX  Human ErbB-2 protein.
XX
XX  Epidermal growth factor receptor; EGFR; therapy; psoriasis; carcinoma;
XX  cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human;
XX  receptor; ErbB-2.
XX
XX  Homo sapiens.
XX
XX  WO2003014159-A1.
XX
XX  20-FEB-2003.
XX
XX  05 AUG 2002; 2002WO-AU001042.
XX
XX  03-AUG-2001; 2001AU-00006927.
XX
XX  03-AUG-2001; 2001AU-00006928.
XX
XX  01-NOV-2001; 2001US-0335333P.
XX
XX  01-NOV-2001; 2001US-0336560P.
XX
XX  31-MAY-2002; 2002AU-00002731.
XX
XX  11-JUN-2002; 2002US-0388171P.
XX
XX  (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX  (BIOM-) BIOMOLECULAR RES INST LTD.
XX  (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX  (LUDW-) LUDWIG INST CANCER RES.
XX
XX  Adams TE, Burgess AW, Elleman TC, Garrett TPJ, Jorissen RN;
XX  Lou M, Lovrecz GO, Mckern NM, Nice EC, Ward CW;
XX  WPI; 2003-268181/26.
XX
XX  Selecting or designing compounds that interact with or inhibit formation
XX  of active dimers of the EGF receptor family, and useful for the
XX  prevention and treatment of disorders, such as psoriasis and cancer of
XX  the breast, brain or colon.
XX
XX  Disclosure; Fig 1; 354pp; English.
XX
XX  The invention relates to a method of selecting or designing a compound
XX  that interacts with or inhibits the formation of active dimers of a
XX  receptor of the epidermal growth factor receptor (EGFR) family. The
XX  methods and compositions of the invention are useful for the prevention
XX  and treatment of disorders associated with signalling by a molecule of
XX  the EGFR family such as psoriasis and cancer of the pancreas, breast,
XX  brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma,
XX  rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and
XX  glioblastomas. The present sequence is human ErbB-2 protein. This
XX  sequence is used to illustrate the method of the invention
XX
XX  Sequence 509 AA;
Query Match      97.0%; Score 128; DB 6; Length 509;
Best Local Similarity 95.8%; Pred. No. 9.1e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 PLHNQEVTAEDGTQCEKCKPCA 24
        |||||||
Db      295 PLHNQEVTAEDGTQCEKCKPCA 318
|||||
RESULT 31
AAE36793
ID  AAE36793 standard; protein; 509 AA.
AC  AAE36793;
XX
XX  01-JUL-2004 (first entry)
XX
XX  Human ErbB2 polypeptide ectodomain fragment.
XX
XX  ErbB2; EGF receptor; ErbB1; ErbB3; ErbB4; cytostatic; human;
XX  protein co-ordinate data.
XX
XX  Homo sapiens.
XX
XX  WO2004031232-A1.
XX
XX  15-APR-2004.
XX
XX  06-OCT-2003; 2003WO-AU001310.
XX
XX  04-OCT-2002; 2002AU-00951853.
XX
XX  (CSIR ) COMMONWEALTH SCI & IND RES ORG.
XX  (LUDW-) LUDWIG INST CANCER RES.
XX  (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX  Garrett TPJ, Elleman TC, Adams TE, Burgess AW, Jorissen RN;
XX  Lou M, Lovrecz GO, Mckern NM, Ward CW;
XX  WPI; 2004-347960/32.
XX
XX  Identifying and designing compounds interacting with ErbB2, used in
XX  diagnosing diseases, involves assessing stereochemical complementarity
XX  between three-dimensional structure of amino acids 1-509 of ErbB2
XX  polypeptide and candidate compound.
XX
XX  Disclosure; SEQ ID NO 1; 148pp; English.
XX
XX  There invention relates to a method for identifying a potential modulator
XX  compound for ErbB2 which involves assessing the stereochemical
XX  complementarity of a three-dimensional structure of amino acids 1-509 of
XX  ErbB2 polypeptide or their subsets and a region of the three-dimensional
XX  structure of a candidate compound and selecting a compound on the basis
XX  of the stereochemical complementarity. Identifying a potential modulator
XX  compound for ErbB2 or the method of modulating ErbB2 further comprises
XX  synthesizing or obtaining a candidate compound assessed as possessing
XX  stereochemical complementarity with a topographical region of the three-
XX  dimensional structure, and determining the ability of the candidate
XX  compound to interact with and/or modulate the activity of ErbB2. The
XX  subset of amino acids is selected from at least one of the CR1 domain,
XX  the potential CR1 loop docking site between the L1, CR1 and L2 domains,
XX  the CR1-L2 hinge region, the regions of the L1 and L2 domains that
XX  contact each other in a closed conformation, and defines at least a part
XX  of the heterodimerization surface with another member of the EGF receptor
XX  family that is selected from the group consisting of ErbB1 (EGF
XX  receptor), ErbB3 and ErbB4. The method is useful for screening for and
XX  designing compounds that interact with ErbB2 or their variants, for
XX  treating diseases such as cancer, melanoma, rhabdomyosarcoma,
XX  mesothelioma and glioblastoma. The present sequence represents the
XX  ectodomain of human ErbB2 protein.
XX
XX  Sequence 509 AA;
Query Match      97.0%; Score 128; DB 8; Length 509;
Best Local Similarity 95.8%; Pred. No. 9.1e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 PLHNQEVTAEDGTQCEKCKPCA 24
        |||||||
Db      295 PLHNQEVTAEDGTQCEKCKPCA 318
|||||
RESULT 31
```

ADT50878
 ID ADT50878 standard; protein; 575 AA.
 XX
 AC ADT50878;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Cancer related protein sequence #41.
 XX
 DE cytostatic; gene therapy; vaccine; diagnosis; breast; colon; lung;
 KW ovarian; prostate; cancer.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO2004092338-A2.
 XX
 PD 28-OCT-2004.
 XX
 PF 12-APR-2004; 2004WO-US011104.
 XX
 PR 11-APR-2003; 2003US-0462399P.
 PR 01-JUL-2003; 2003US-0484333P.
 XX
 PA (DIAD-) DIADEXUS INC.
 XX
 PI Macina RA, Turner LR, Sun Y, Tam A;
 XX
 DR WPI; 2004-766851/75.
 XX
 XX New cancer specific nucleic acid (CaSNA) molecules, useful for
 PT diagnosing, monitoring the presence of, or treating a patient with
 PT breast, colon, lung, ovarian, or prostate cancer.
 PT
 XX
 PS Claim 12; SEQ ID NO 182; 891pp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule (I)
 CC selectively hybridizing to, or comprising at least 95% sequence identity
 CC to, any of the 362 nucleotide sequences fully defined in the
 CC specification. The nucleic acid molecules and polypeptides are useful for
 CC diagnosing, monitoring the presence of, or treating a patient with
 CC breast, colon, lung, ovarian, or prostate cancer. This sequence
 CC corresponds to a protein of the invention.
 CC
 XX
 SQ Sequence 575 AA;
 Query Match 97.0%; Score 128; DB 8; Length 575;
 Best Local Similarity 95.8%; Pred. No. 1e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
 DB 316 PLHNQEVTAEDGTQRAEKCCKPCA 339
 |||||
 RESULT 32
 ADY28117
 ID ADY28117 standard; protein; 575 AA.
 XX
 AC ADY28117;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Receptor tyrosine kinase protein - SEQ ID 7.
 XX
 KW receptor tyrosine kinase; angiogenesis; cell proliferation;
 KW cell migration; cell growth; metastasis; cancer; cytosstatic;
 KW rheumatoid arthritis; antiarthritic; antirheumatic; multiple sclerosis;
 KW neuroprotective; inflammation; antiinflammatory; uveitis;
 KW ophthalmological; ocular inflammation; atherosclerosis;
 KW arterioisclerotic; hemangioma; diabetes mellitus;
 KW inflammatory bowel disease; gastrointestinal-gen.; Crohns disease;
 KW psoriasis; antipsoriatic; Alzheimers disease; neuroprotective; nootropic;
 KW systemic lupus erythematosus; restenosis; vasotropic; asthma;

KW antiasthmatic; receptor tyrosine kinase.
 XX
 OS Unidentified.
 XX
 PN WO2005016966-A2.
 XX
 PD 24-FEB-2005.
 XX
 PF 14-MAY-2004; 2004WO-US015056.
 XX
 PR 16-MAY-2003; 2003US-0471141P.
 XX
 PA (RECE-) RECEPTOR BIOLOGIX INC.
 XX (JINP/) JIN P.
 XX
 PI Jin P, Shepard HM, Clinton GM, Lackey DB;
 XX
 DR WPI; 2005-182332/19.
 XX
 XX New receptor tyrosine kinase isoforms (such as TEK (TIE-2)), useful for
 PT treating a disease or condition, e.g. cancers, or inflammatory,
 PT infectious, immune, or neurodegenerative diseases.
 PT
 XX
 PS Claim 2; SEQ ID NO 7; 105pp; English.
 XX
 CC The invention comprises the amino acid sequence of a number of receptor
 CC tyrosine kinase proteins which are useful for identifying drugs that
 CC modulate the receptor and for inhibiting angiogenesis, cell
 CC proliferation, cell migration, tumor cell growth or tumor cell
 CC metastasis. The receptor tyrosine kinase proteins of the invention are
 CC useful for treating cancers, rheumatoid arthritis, multiple sclerosis and
 CC posterior intraocular inflammation, uveitic disorders, ocular surface
 CC inflammatory disorders, neovascular disease, proliferative
 CC vitreoretinopathy, atherosclerosis, hemangioma, diabetes mellitus,
 CC inflammatory bowel disease, Crohn's disease, psoriasis, Alzheimer's
 CC disease, lupus, vascular stenosis, restenosis, inflammatory joint
 CC disease, urinary obstructive syndromes, and asthma. The present amino
 CC acid sequence represents a receptor tyrosine kinase protein of the
 CC invention. NOTE: The present sequence is not shown in the specification,
 CC but has been retrieved from the WIPO website.
 XX
 SQ Sequence 575 AA;
 Query Match 97.0%; Score 128; DB 9; Length 575;
 Best Local Similarity 95.8%; Pred. No. 1e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
 DB 316 PLHNQEVTAEDGTQRAEKCCKPCA 339
 |||||
 RESULT 33
 ADZ47797
 ID ADZ47797 standard; protein; 575 AA.
 XX
 AC ADZ47797;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Amino acid sequence for human ErbB-2 variant II.
 XX
 KW epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
 KW prognosis; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Active-site 505..575
 FT /note= "Given as SEQ ID No:6 in the specification"
 XX
 PN WO2005033133-A2.
 XX

PD 14-APR-2005.
 XX
 PF 04-OCT-2004; 2004WO-US030903.
 XX
 PR 03-OCT-2003; 2003US-0507953P.
 PR 10-NOV-2003; 2003US-0518321P.
 PR 09-AUG-2004; 2004US-0599583P.
 PR 07-SEP-2004; 2004US-0607326P.
 XX
 PA (COMP-) COMPUGEN LTD.
 PA (COMP-) COMPUGEN INC.
 XX
 PI Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
 PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
 XX
 DR WPI; 2005-285403/29.
 DR N-PSDB; ADZ47796.
 XX
 XX New isolated polynucleotide encoding at least an active portion of an
 PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
 PT aberrant expression or activity of the ErbB-2 polypeptides, such as
 PT cancer.
 XX
 XX Claim 19; SEQ ID NO 4; 246pp; English.
 XX
 CC The invention relates to the isolation of polynucleotide sequences
 CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
 CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
 CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
 CC treatment of ErbB-2 related cancer. The sequences, methods, and
 CC compositions of the present invention are useful for diagnosing,
 CC prognosing, and/or treating diseases or conditions associated with
 CC aberrant expression or activity of the ErbB-2 polypeptides, such as
 CC cancer. This sequence represents human ErbB-2 variant II.
 XX
 XX SQ Sequence 575 AA;
 Query Match 97.0%; Score 128; DB 9; Length 575;
 Best Local Similarity 95.8%; Pred. No. 1e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PLHNQEVTAEDGTQRAEKCKPCA 24
 Db 316 PLHNQEVTAEDGTQRAEKCKPCA 339
 RESULT 34
 ADZ47809
 ID ADZ47809 standard; protein; 614 AA.
 XX
 AC ADZ47809;
 XX
 DT 30-JUN-2005 (first entry)
 XX
 DE Amino acid sequence for human ErbB-2 variant V.
 XX
 KW epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
 KW prognosis; cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2005033133-A2.
 XX
 PD 14-APR-2005.
 XX
 PF 04-OCT-2004; 2004WO-US030903.
 XX
 PR 03-OCT-2003; 2003US-0507953P.
 PR 10-NOV-2003; 2003US-0518321P.
 PR 09-AUG-2004; 2004US-0599583P.
 PR 07-SEP-2004; 2004US-0607326P.
 XX
 PA (COMP-) COMPUGEN LTD.
 PA (COMP-) COMPUGEN INC.

PA (COMP-) COMPUGEN INC.
 XX
 PF Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
 PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
 XX
 DR WPI; 2005-285403/29.
 DR N-PSDB; ADZ47808.
 XX
 XX New isolated polynucleotide encoding at least an active portion of an
 PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
 PT aberrant expression or activity of the ErbB-2 polypeptides, such as
 PT cancer.
 XX
 XX Claim 41; SEQ ID NO 16; 246pp; English.
 XX
 CC The invention relates to the isolation of polynucleotide sequences
 CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
 CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
 CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
 CC treatment of ErbB-2 related cancer. The sequences, methods, and
 CC compositions of the present invention are useful for diagnosing,
 CC prognosing, and/or treating diseases or conditions associated with
 CC aberrant expression or activity of the ErbB-2 polypeptides, such as
 CC cancer. This sequence represents human ErbB-2 variant V.
 XX
 XX SQ Sequence 614 AA;
 Query Match 97.0%; Score 128; DB 9; Length 614;
 Best Local Similarity 95.8%; Pred. No. 1e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 PLHNQEVTAEDGTQRAEKCKPCA 24
 Db 316 PLHNQEVTAEDGTQRAEKCKPCA 339
 RESULT 35
 AAR08222
 ID AAR08222 standard; protein; 624 AA.
 XX
 AC AAR08222;
 XX
 DT 06-MAR-1991 (first entry)
 XX
 DE Extracellular portion of the human epidermal growth factor receptor 2.
 XX
 KW Human epidermal growth factor receptor 2; HER2; vaccine; cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 22..32
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 74..84
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 113..130
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 187..197
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 305..315
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 327..353
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 375..385
 FT /label= epitope
 FT /note= "potential T-cell epitope"
 FT Region 398..408

XX Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
 PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
 XX WPI; 2005-285403/29.
 DR New isolated polynucleotide encoding at least an active portion of an
 XX ErbB-2 polypeptide, useful for diagnosing or treating diseases with
 PT aberrant expression or activity of the ErbB-2 polypeptides, such as
 PT cancer.
 XX Disclosure; Fig 4; 246pp; English.
 PS
 XX The invention relates to the isolation of polynucleotide sequences
 CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
 CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
 CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
 CC treatment of ErbB-2 related cancer. The sequences, methods, and
 CC compositions of the present invention are useful for diagnosing,
 CC prognosing, and/or treating diseases or conditions associated with
 CC aberrant expression or activity of the ErbB-2 polypeptides, such as
 CC cancer. This sequence represents human 100 KDa ErbB-2 variant
 CC polypeptide.
 XX
 XX SQ Sequence 633 AA;
 Query Match 97.0%; Score 128; DB 9; Length 633;
 Best Local Similarity 95.8%; Pred. No. 1.2e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
 DB 316 PLHNQEVTAEDGTQRCCKSPCA 339
 RESULT 38
 AAB60408
 ID AAB60408 standard; protein; 645 AA.
 XX
 AC AAB60408;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human ErbB2 oncoprotein, SEQ ID NO:13.
 XX
 KW Anti-ErbB2 monoclonal antibody 2C4; HER2; mouse; murine; humanised; VL;
 KW light chain variable region; cancer; cytostatic; EGFR-expressing cancer;
 KW epidermal growth factor receptor; colon cancer; rectal cancer; tumour;
 KW colorectal cancer; non-small cell lung cancer; metastatic breast cancer;
 KW affinity purification.
 XX
 OS Homo sapiens.
 XX
 PN WO200100245-A2.
 XX
 PD 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-US017366.
 XX
 PR 25-JUN-1999; 99US-0141316P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Adams CW, Presta LG, Sliwkowsky M;
 PI WPI; 2001-080862/09.
 DR
 XX Treating cancer in a human, where the cancer expresses epidermal growth
 PT factor receptor (EGFR), comprises administering an antibody which binds
 PT ErbB2.
 XX
 XX Example 1; Fig 1A; 89pp; English.
 PS
 XX

CC The invention relates to a method for treating cancer in a human patient,
 CC wherein the cancer expresses epidermal growth factor receptor (EGFR),
 CC comprising administering an antibody which binds ErbB2 (HER2; AAB60408).
 CC In particular, the anti-ErbB2 antibody is the murine monoclonal antibody
 CC 2C4 (AAB60396, AAB60397) or a humanised version of 2C4 (AAB60398,
 CC AAB60399). The invention also encompasses an isolated nucleic acid
 CC encoding a humanised ErbB2-binding antibody; vectors and host cells
 CC comprising such nucleic acids; the recombinant production of a humanised
 CC ErbB2-binding antibody; and an immunoconjugate comprising a humanised
 CC ErbB2-binding antibody and a cytotoxic drug. The ErbB2-binding antibodies
 CC act by antagonising ErbB receptors, and as inhibitors of transforming
 CC growth factor alpha (TGF-alpha)-activated mitogen activated protein
 CC kinase (MAPK). The method of the invention is used for treating cancer,
 CC especially colon cancer, rectal cancer, colorectal cancer, lung cancer,
 CC (especially non-small cell lung cancer), or breast cancer (especially
 CC metastatic breast cancer). The antibodies may also have non-therapeutic
 CC uses e.g., as affinity purification agents. Using an antibody which binds
 CC to ErbB2 to treat cancer is preferable to the use of EGFR-targeted
 CC drugs, as EGFR is also highly expressed in other tissues such as the
 CC liver and skin, where the active drug will also bind, with skin toxicity
 CC having been observed for EGFR-targeted drugs. Antibodies which bind
 CC ErbB2 are anticipated to have a better safety profile than such drugs.
 CC The present sequence represents human ErbB2
 XX
 XX SQ Sequence 645 AA;
 Query Match 97.0%; Score 128; DB 4; Length 645;
 Best Local Similarity 95.8%; Pred. No. 1.2e-10;
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
 DB 316 PLHNQEVTAEDGTQRCCKSPCA 339
 RESULT 39
 AAB61593
 ID AAB61593 standard; protein; 645 AA.
 XX
 AC AAB61593;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human ErbB2 extracellular domain.
 XX
 KW Human; ErbB2; cytostatic; prostate cancer; receptor tyrosine kinase;
 KW antibody; ErbB receptor; monoclonal antibody 2C4; variable light chain.
 XX
 OS Homo sapiens.
 XX
 PN WO200100238-A1.
 XX
 XX 04-JAN-2001.
 XX
 PF 23-JUN-2000; 2000WO-US017423.
 XX
 PR 25-JUN-1999; 99US-0141315P.
 XX
 XX (GETH) GENENTECH INC.
 PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX
 XX Agus DB, Scher HI, Sliwkowski MX;
 XX WPI; 2001-159131/16.
 DR
 XX Treating prostate cancer in a human comprises administering an antibody
 PT which binds ErbB2 and blocks ligand activation of an ErbB receptor.
 XX
 PS Disclosure; Fig 1; 93pp; English.
 XX
 XX The ErbB family of receptor tyrosine kinases are important mediators of
 CC cell growth, differentiation and survival. The receptor family includes
 CC four distinct members including Epidermal Growth Factor Receptor (EGFR) or

CC ErbB1), HER2 (ErbB2 or p185^{neu}), HER3 (ErbB3) and Her4 (ErbB4 or tyro2).
CC The present invention relates to a method for treating prostate cancer.
CC The method comprises administering an antibody which binds ErbB2 and
CC blocks ligand activation of an ErbB receptor. Preferably, the antibody
CC blocks binding of monoclonal antibody 2C4 to ErbB2 and/or blocks TGF-
CC alpha activation of mitogen-activated protein kinase (MAPK). The present
CC sequence is the extracellular domain of human ErbB2

XX SQ Sequence 645 AA;

Query Match 97.0%; Score 128; DB 4; Length 645;
Best Local Similarity 95.8%; Pred. No. 1.2e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPKCA 24
|||||
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339

RESULT 40

ABG70753
ID ABG70753 standard; protein; 645 AA.

XX AC ABG70753;

XX DT 28-NOV-2002 (first entry)

XX DE Human HER2 receptor extracellular domain.

XX KW Human; HER2; analyte; interfering substance; serum; HERCEPTIN; therapy;
KW anti-HER2; antibody; plasma; HER2; ErbB2; ErbB2 receptor;
KW extracellular domain; ECD; epitope; cancer.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..21
FT /label= Signal_peptide

XX PN US2002090662-A1.

XX PD 11-JUL-2002.

XX PF 01-AUG-2001; 2001US-00921161.

XX PR 15-AUG-2000; 2000US-0225433P.

XX PA (RALP/) RALPH P.

XX PI Ralph P;

XX DR WPI; 2002-697507/75.

XX PT Determining an analyte in the presence of an interfering substance,
PT comprises contacting a sample with an antibody recognizing analyte coated
PT surface and interfering substance, and measuring unbound and bound
PT analyte.

XX PS Example 1; Fig 1; 16pp; English.

XX CC The invention discloses a method for determining the amount of an analyte
CC in a fluid sample in the presence of an interfering substance. The method
CC comprises contacting a solid surface, dual-coated with an antibody
CC recognising a free analyte and a second antibody recognising an
CC interfering substance when bound to the analyte, with a fluid sample and
CC then determining the total amount of free analyte and analyte bound to
CC the interfering substance. The example in this specification discloses
CC the quantitative determination of serum HERCEPTIN levels in patients
CC undergoing HERCEPTIN therapy. The method accurately determines the amount
CC of an anti-HER2 antibody in serum or plasma in the presence of an HER2
CC (also referred to as ErbB2 and ErbB2 receptor, not defined) extracellular
CC domain (ECD). The labelled secondary antibody recognises the anti-HER2
CC antibody at an epitope different from that recognised by the first

CC antibody, as well as different from that recognised by the HER2 ECD. The
CC method is useful for accurately determining the amount of an antibody,
CC anti-HER2, that is circulating in a fluid sample (serum or plasma)
CC derived from a cancer patient undergoing anti-HER2 therapy, in the
CC presence of an interfering substance (the ECD) of the HER2 oncogene. The
CC method prevents loss of detection in the qualitative assays and an
CC underestimation in the quantitative assays. The sequence presented is the
CC human HER2 receptor extracellular domain

XX SQ Sequence 645 AA;

Query Match 97.0%; Score 128; DB 5; Length 645;
Best Local Similarity 95.8%; Pred. No. 1.2e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPKCA 24
|||||
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339

Search completed: December 3, 2005, 07:43:42
Job time : 156.545 secs

ALIGNMENTS

RESULT 1
US-09-630-155-2
; Sequence 2, Application US/09630155
; Patent No. 6414130
; GENERAL INFORMATION:
; APPLICANT: Doherty, Joni Kristin and Gail M. Clinton
; TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
; STREET: 1501 Fourth Avenue, 2600 Century Square
; CITY: Seattle
; STATE: Washington
; COUNTRY: U.S.A.
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: PC compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; FILING DATE: 16-Jan-2001
; APPLICATION NUMBER: US/09/630,155
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Davison, Barry L.
; REGISTRATION NUMBER: 47,309
; REFERENCE/DOCKET NUMBER: 49321-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206 628-7621
; TELEFAX: 206 628-7699
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 419
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: polypeptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-630-155-2

Query Match 97.0%; Score 128; DB 2; Length 419;
Best Local Similarity 95.8%; Pred. No. 2.2e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339
|||||
; GENERAL INFORMATION:
; APPLICANT: Hudziak, Robert M.
; APPLICANT: Shepard, H. Michael
; TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,108
; FILING DATE: 14-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/422108
; FILING DATE: 14-Apr-1995
; APPLICATION NUMBER: 08/355460
; FILING DATE: 13-DEC-1994
; PRIOR APPLICATION DATA:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,108
; FILING DATE: 14-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/355460
; FILING DATE: 13-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/048346
; FILING DATE: 15-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/354319
; FILING DATE: 19-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 554C2D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 624 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-422-108-1

Query Match 97.0%; Score 128; DB 2; Length 624;
Best Local Similarity 95.8%; Pred. No. 3.5e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 295 PLHNQEVTAEDGTQRAEKCCKPCA 318
|||||
; GENERAL INFORMATION:
; APPLICANT: Hudziak, Robert M.
; APPLICANT: Shepard, H. Michael
; TITLE OF INVENTION: HER2 EXTRACELLULAR DOMAIN
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,734
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 08/422108
; FILING DATE: 14-Apr-1995
; APPLICATION NUMBER: 08/355460
; FILING DATE: 13-DEC-1994
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/048346
FILING DATE: 15-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/354319
FILING DATE: 19-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 554C2D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 624 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-422-734-1

Query Match 97.0%; Score 128; DB 2; Length 624;
Best Local Similarity 95.8%; Pred. No. 3.5e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPKCA 24
|||||
Db 295 PLHNQEVTAEDGTQRAEKCKPKCA 318

RESULT 4
US-09-602-812A-13
Sequence 13, Application US/09602812A
Patent No. 6949245
GENERAL INFORMATION:
APPLICANT: Adams, Camellia W.
APPLICANT: Presta, Leonard G.
APPLICANT: Sliwowski, Mark X.
TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies
TITLE OF INVENTION: Anti-ErbB2 Antibodies
FILE REFERENCE: P1467R2
CURRENT APPLICATION NUMBER: US/09/602,812A
CURRENT FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/141,316
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 13
LENGTH: 645
TYPE: PRT
ORGANISM: Homo sapiens
US-09-602-812A-13

Query Match 97.0%; Score 128; DB 2; Length 645;
Best Local Similarity 95.8%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPKCA 24
|||||
Db 316 PLHNQEVTAEDGTQRAEKCKPKCA 339

RESULT 5
US-09-146-283-4
Sequence 4, Application US/09146283
Patent No. 5976546
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Compositions
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250

CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,283
FILING DATE: 03-SEPT-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 782 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: homo sapiens
INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
US-09-146-283-4

Query Match 97.0%; Score 128; DB 1; Length 782;
Best Local Similarity 95.8%; Pred. No. 4.5e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPKCA 24
|||||
Db 316 PLHNQEVTAEDGTQRAEKCKPKCA 339

RESULT 6
US-08-579-823A-4
Sequence 4, Application US/08579823A
Patent No. 6080409
GENERAL INFORMATION:
APPLICANT: Laus, Reiner
APPLICANT: Ruegg, Curtis L.
APPLICANT: Wu, Hongyu
TITLE OF INVENTION: Immunostimulatory Composition and Method
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave. Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579,823A
FILING DATE: 03-DEC-1998
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Judge, Linda R.
REGISTRATION NUMBER: 42,702
REFERENCE/DOCKET NUMBER: 7636-0010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880

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/ TELEFAX: 650-324-0960
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 782 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapiens
/ INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
/ US-08-579-823A-4

Query Match 97.0%; Score 128; DB 2; Length 782;
Best Local Similarity 95.8%; Pred. No. 4.5e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 7
US-09-344-195-4
; Sequence 4, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; RUEGG, CURTIS L.
; WU, HONGYU
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-344-195-4

Query Match 97.0%; Score 128; DB 2; Length 782;
Best Local Similarity 95.8%; Pred. No. 4.5e-11;

/ TELEFAX: 650-324-0960
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 782 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: homo sapiens
/ INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
/ US-08-579-823A-4

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 8
US-08-467-083-68
; Sequence 68, Application US/08467083
; Patent No. 5726023
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-467-083-68

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 9
US-08-414-417B-68
; Sequence 68, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
```


ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-414-417B-68

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTORAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTORCEKCKSPCA 339

RESULT 10
US-08-484-438-8
Sequence 8, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993

CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-8

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTORAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTORCEKCKSPCA 339

RESULT 11
US-08-486-348A-68
Sequence 68, Application US/08486348A
Patent No. 5846538
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-486-348A-68

Query Match 97.0%; Score 128; DB 1; Length 1255;

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Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  PLHNQEVTAEDGTQRAEKCKPKCA 24
      |||||||
Db      316 PLHNQEVTAEDGTQRCCKCKPKCA 339

RESULT 12
US-08-625-101-2
; Sequence 2, Application US/08625101
; Patent No. 5863445
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-625-101-2

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  PLHNQEVTAEDGTQRAEKCKPKCA 24
      |||||||
Db      316 PLHNQEVTAEDGTQRCCKCKPKCA 339

RESULT 13
US-08-468-545B-68
; Sequence 68, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: seed and Berry LLP

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/354,533
/ FILING DATE: 15-Jul-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C9
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 68:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1255 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 68:

US-09-354-533-68
Query Match 97.0%; Score 128; DB 2; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 19

US-09-441-411-6
/ Sequence 6, Application US/09441411
/ Patent No. 6734172
/ GENERAL INFORMATION:
/ APPLICANT: Scholler, Nathalie B.
/ APPLICANT: Disis, Mary L.
/ APPLICANT: Hellstrom, Ingegerd
/ APPLICANT: Hellstrom, Karl Erik
/ TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
/ FILE REFERENCE: 730033.409
/ CURRENT APPLICATION NUMBER: US/09/441,411
/ CURRENT FILING DATE: 1999-11-16
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1255
/ TYPE: PRT
/ ORGANISM: Homo sapiens

US-09-441-411-6

Query Match 97.0%; Score 128; DB 2; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 20

US-09-167-516-2
/ Sequence 2, Application US/09167516
/ Patent No. 6953573
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disis, Mary L.
/ TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
/ TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
/ TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
/ TITLE OF INVENTION: ONCOGENE IS ASSOCIATED

/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED and BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/167,516
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/625,101
/ FILING DATE: 01-APR-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Sharkey, Richard G.
/ REGISTRATION NUMBER: 32,629
/ REFERENCE/DOCKET NUMBER: 920010.448C7
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1255 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-167-516-2

Query Match 97.0%; Score 128; DB 2; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

RESULT 21

US-08-467-083-56
/ Sequence 56, Application US/08467083
/ Patent No. 5726023
/ GENERAL INFORMATION:
/ APPLICANT: Cheever, Martin A.
/ APPLICANT: Disis, Mary L.
/ TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
/ TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
/ TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
/ NUMBER OF SEQUENCES: 68
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Seed and Berry
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: US
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/467,083
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/414,417

US-08-467-083-56

Query Match 97.0%; Score 128; DB 2; Length 1255;
Best Local Similarity 95.8%; Pred. No. 7.6e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCCKPCA 339

;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sharkey, Richard G.
;; REGISTRATION NUMBER: 32,629
;; REFERENCE/DOCKET NUMBER: 920010.448C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; TELEX: 3723836 SEEDANBERRY
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
US-08-467-083-56

Query Match 53.8%; Score 71; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NQEVTAEDGTORAEK 18
Db 1 NQEVTAEDGTORCEK 15

RESULT 22

US-08-414-417B-56
; Sequence 56, Application US/08414417B
; Patent No. 5801005

;; GENERAL INFORMATION:
;; APPLICANT: Cheever, Martin A.
;; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,417B
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sharkey, Richard G.
;; REGISTRATION NUMBER: 32,629
;; REFERENCE/DOCKET NUMBER: 920010.448C2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear

US-08-414-417B-56

Query Match 53.8%; Score 71; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NQEVTAEDGTORAEK 18

Db 1 NQEVTAEDGTORCEK 15

RESULT 23

US-08-486-348A-56
; Sequence 56, Application US/08486348A
; Patent No. 5846538

;; GENERAL INFORMATION:
;; APPLICANT: Cheever, Martin A.
;; APPLICANT: Disis, Mary L.
;; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,348A
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sharkey, Richard G.
;; REGISTRATION NUMBER: 32,629
;; REFERENCE/DOCKET NUMBER: 920010.448C6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 622-4900
;; TELEFAX: (206) 682-6031
;; INFORMATION FOR SEQ ID NO: 56:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear

US-08-486-348A-56

Query Match 53.8%; Score 71; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NQEVTAEDGTORAEK 18
Db 1 NQEVTAEDGTORCEK 15

RESULT 24

US-08-468-545B-56
; Sequence 56, Application US/08468545B
; Patent No. 5876712

;; GENERAL INFORMATION:
;; APPLICANT: Cheever, Martin A.
;; APPLICANT: Disis, Mary L.
;; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
;; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
;; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
;; NUMBER OF SEQUENCES: 69
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Seed and Berry LLP
;; STREET: 6300 Columbia Center, 701 Fifth Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: US
;; ZIP: 98104-7092

Query Match 53.8%; Score 71; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NQEVTAEDGTORAEK 18

[illegible]

```
;
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,083
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/414,417
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; TELEX: 3723836 SEEDANBERRY
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-467-083-60
;
; Query Match 47.7%; Score 63; DB 1; Length 18;
; Best Local Similarity 91.7%; Pred. No. 0.0054;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 13 TORAEKCSKPCA 24
; DB 1 TORCEKCSKPCA 12
;
; RESULT 28
; US-08-414-417B-60
; Sequence 60, Application US/08414417B
; Patent No. 5801005
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-414-417B-60
;
; Query Match 47.7%; Score 63; DB 1; Length 18;
; Best Local Similarity 91.7%; Pred. No. 0.0054;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 13 TORAEKCSKPCA 24
; DB 1 TORCEKCSKPCA 12
;
; RESULT 29
; US-08-486-348A-60
; Sequence 60, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-486-348A-60
;
; Query Match 47.7%; Score 63; DB 1; Length 18;
; Best Local Similarity 91.7%; Pred. No. 0.0054;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 13 TORAEKCSKPCA 24
; DB 1 TORCEKCSKPCA 12
;
; RESULT 30
; US-08-486-348A-60
; Sequence 60, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
; US-08-486-348A-60
;
; Query Match 47.7%; Score 63; DB 1; Length 18;
; Best Local Similarity 91.7%; Pred. No. 0.0054;
; Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
;
; QY 13 TORAEKCSKPCA 24
; DB 1 TORCEKCSKPCA 12
;
; RESULT 31
; US-08-486-348A-60
; Sequence 60, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,417B
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
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RESULT 30
US-08-468-545B-60
; Sequence 60, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C5
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-468-545B-60
Query Match 47.7%; Score 63; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TQRAEKCSKPCA 24
||| |||||||
Db 1 TQCEKCSKPCA 12

RESULT 31
US-09-632-036f-60
; Sequence 60, Application US/0846680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-354-533-60
Query Match 47.7%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TQRAEKCSKPCA 24
||| |||||||
Db 1 TQCEKCSKPCA 12

RESULT 32
US-09-354-533-60
; Sequence 60, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-354-533-60
Query Match 47.7%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TQRAEKCSKPCA 24
||| |||||||
Db 1 TQCEKCSKPCA 12

RESULT 33
US-09-354-533-60
; Sequence 60, Application US/09354533
; Patent No. 6664370
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-354-533-60
Query Match 47.7%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TQRAEKCSKPCA 24
||| |||||||
Db 1 TQCEKCSKPCA 12
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Query Match 47.7%; Score 63; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.0054;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 TORAEKCKSPCA 24
Db 1 TORCEKCKPCA 12

RESULT 33
US-08-403-459-32
; Sequence 32, Application US/08403459
; Patent No. 6514942
; GENERAL INFORMATION:
; APPLICANT: Ioannides, Constantin G.
; APPLICANT: Fisk, Bryan A.
; APPLICANT: Ioannides, Maria G.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING
; TITLE OF INVENTION: T-LYMPHOCYTES
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/403.459
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSC:390/KIT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-403-459-32

Query Match 40.2%; Score 53; DB 2; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.12;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NOEVTAEQTQR 15
Db 1 NOEVTAWDGTQR 12

RESULT 34
US-09-055-095-3
; Sequence 3, Application US/09055095
; Patent No. 5945308
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Sather, Susan
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,095
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0500 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1902984
US-09-055-095-3

Query Match 39.4%; Score 52; DB 1; Length 273;
Best Local Similarity 36.4%; Pred. No. 5.4;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 LHNQVTAEDGTORAEKCKSPC 23
Db 123 LHHQNLNLQETLKRVCNCSAPC 144

RESULT 35
US-08-809-494A-6
; Sequence 6, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-809-494A-6

Query Match 39.4%; Score 52; DB 1; Length 273;
Best Local Similarity 36.4%; Pred. No. 5.4;
Matches 8; Conservative 5; Mismatches 9; Indels 9; Gaps 0;

QY 2 LHNQEVTAEDGTQRAEKCKSPC 23
Db 123 LHHQNLNLQETLKRVCNSAPC 144

RESULT 36
US-09-352-302-6
; Sequence 6, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Masaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/352,302
; FILING DATE: 12-JUL-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 273 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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; MOLECULE TYPE: protein
; US-09-352-302-6

Query Match 39.4%; Score 52; DB 2; Length 273;
Best Local Similarity 36.4%; Pred. No. 5.4;
Matches 8; Conservative 5; Mismatches 9; Indels 9; Gaps 0;

QY 2 LHNQEVTAEDGTQRAEKCKSPC 23
Db 123 LHHQNLNLQETLKRVCNSAPC 144

RESULT 37
US-09-949-016-11494
; Sequence 11494, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11494
; LENGTH: 746
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-11494

Query Match 39.4%; Score 52; DB 2; Length 746;
Best Local Similarity 47.6%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 7; Indels 7; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSK 21
Db 243 PLESQSAEGMSQRCCECGK 263

RESULT 38
US-09-902-540-9732
; Sequence 9732, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9732
; LENGTH: 2324
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-9732

Query Match 39.4%; Score 52; DB 2; Length 2324;
Best Local Similarity 45.5%; Pred. No. 60;
Matches 10; Conservative 3; Mismatches 9; Indels 9; Gaps 0;

QY 3 HNQEVTAEADGTQRAEKCKPCA 24
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Db 494 HRRVVAADGAELAEERLRKPA 515

RESULT 39

US-08-159-339A-285
; Sequence 285, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esben
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-285

Query Match 37.1%; Score 49; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 GTQRAEKCSK 21
Db 1 GTQCEKCSK 10

RESULT 40

US-08-159-339A-285
; Patent No. 5459061
; APPLICANT: SATO, J DENRY;WU, DIANGING;WANG, LIHUA
; TITLE OF INVENTION: HYBRIDOMAS PRODUCING MONOCLONAL ANTIBODIES
; WHICH SPECIFICALLY BIND TO CONTINUOUS EPITOPE ON THE HUMAN EGF
; RECEPTOR AND COMPETE WITH EGF FOR BINDING TO THE EGF RECEPTOR
; NUMBER OF SEQUENCES: 10

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,274
; FILING DATE: 07-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 470,642
; FILING DATE: 26-JAN-1990
; SEQ ID NO:1:
; LENGTH: 76
5459061-1

Query Match 37.1%; Score 49; DB 6; Length 76;
Best Local Similarity 50.0%; Pred. No. 3.7;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 10 EDGTQRAEKCSKPC 23
Db 2 EDGVRKCKCEGPC 15

Search completed: December 3, 2005, 07:49:48
Job time : 37.4545 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:50:00 ; Search time 119.455 Seconds
(without alignments)
83.947 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHQEVTAEDGTQRAEKSKPCA 24

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

-Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published_Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	128	97.0	387	5	US-10-956-373-26
2	128	97.0	419	4	US-10-302-663-2
3	128	97.0	419	4	US-10-344-470-2
4	128	97.0	419	5	US-10-775-204-1811
5	128	97.0	419	5	US-10-846-113A-9
6	128	97.0	509	5	US-10-485-683-2
7	128	97.0	575	5	US-10-956-373-4
8	128	97.0	607	5	US-10-846-113A-7
9	128	97.0	607	6	US-11-021-951-183
10	128	97.0	614	5	US-10-956-373-16
11	128	97.0	633	5	US-10-846-113A-6
12	128	97.0	645	4	US-09-921-161-1
13	128	97.0	645	4	US-10-288-501-13
14	128	97.0	645	5	US-10-608-626-13
15	128	97.0	645	5	US-10-719-310-13
16	128	97.0	645	6	US-11-044-749-13
17	128	97.0	645	6	US-11-154-465-13
18	128	97.0	653	3	US-09-854-356-3
19	128	97.0	678	5	US-10-956-373-2
20	128	97.0	680	5	US-10-846-113A-5
21	128	97.0	685	4	US-10-412-804A-4
22	128	97.0	690	4	US-10-412-804A-11
23	128	97.0	712	3	US-09-854-356-7
24	128	97.0	715	4	US-10-412-804A-10
25	128	97.0	717	5	US-10-956-373-14
26	128	97.0	720	4	US-10-412-804A-6
27	128	97.0	919	3	US-09-854-356-6

28	128	97.0	1006	5	US-10-775-204-1643	Sequence 1643, Ap
29	128	97.0	1253	4	US-10-146-473-72	Sequence 72, Appli
30	128	97.0	1255	3	US-09-811-123-9	Sequence 9, Appli
31	128	97.0	1255	3	US-09-811-115-3	Sequence 3, Appli
32	128	97.0	1255	3	US-09-765-973-2	Sequence 2, Appli
33	128	97.0	1255	3	US-09-354-533-68	Sequence 68, Appli
34	128	97.0	1255	3	US-09-769-508-2	Sequence 2, Appli
35	128	97.0	1255	3	US-09-854-356-1	Sequence 1, Appli
36	128	97.0	1255	3	US-09-930-125-2	Sequence 2, Appli
37	128	97.0	1255	3	US-09-441-411-6	Sequence 6, Appli
38	128	97.0	1255	3	US-09-984-092-4	Sequence 4, Appli
39	128	97.0	1255	4	US-10-207-655-45	Sequence 45, Appli
40	128	97.0	1255	4	US-10-177-293-126	Sequence 126, App
41	128	97.0	1255	4	US-10-207-498-6	Sequence 6, Appli
42	128	97.0	1255	4	US-10-338-730-2	Sequence 2, Appli
43	128	97.0	1255	4	US-10-313-644-2	Sequence 2, Appli
44	128	97.0	1255	4	US-10-322-892-4	Sequence 4, Appli
45	128	97.0	1255	4	US-10-272-437A-28	Sequence 28, Appli
46	128	97.0	1255	4	US-10-117-937-594	Sequence 594, App
47	128	97.0	1255	4	US-10-418-027-3	Sequence 3, Appli
48	128	97.0	1255	4	US-10-394-322A-17	Sequence 17, Appli
49	128	97.0	1255	4	US-10-245-871-553	Sequence 553, App
50	128	97.0	1255	4	US-10-435-696-36	Sequence 36, Appli
51	128	97.0	1255	4	US-10-149-138-4641	Sequence 4641, Ap
52	128	97.0	1255	4	US-10-469-162-3	Sequence 3, Appli
53	128	97.0	1255	4	US-10-253-286-553	Sequence 553, App
54	128	97.0	1255	4	US-10-647-005-68	Sequence 68, Appli
55	128	97.0	1255	4	US-10-149-138-4641	Sequence 4641, Ap
56	128	97.0	1255	4	US-10-441-779C-4	Sequence 4, Appli
57	128	97.0	1255	4	US-10-734-564-126	Sequence 126, App
58	128	97.0	1255	4	US-10-657-022-90	Sequence 90, Appli
59	128	97.0	1255	5	US-10-762-128-6	Sequence 6, Appli
60	128	97.0	1255	5	US-10-484-067-1	Sequence 1, Appli
61	128	97.0	1255	5	US-10-723-860-9	Sequence 9, Appli
62	128	97.0	1255	5	US-10-615-343-17	Sequence 17, Appli
63	128	97.0	1255	5	US-10-794-514A-1	Sequence 1, Appli
64	128	97.0	1255	5	US-10-871-708-9	Sequence 9, Appli
65	128	97.0	1255	5	US-10-983-340-17	Sequence 17, Appli
66	128	97.0	1255	5	US-10-846-113A-27	Sequence 27, Appli
67	128	97.0	1255	6	US-11-067-064-594	Sequence 594, App
68	128	97.0	1255	6	US-11-121-347-68	Sequence 68, Appli
69	128	97.0	1255	6	US-11-037-713-12	Sequence 12, Appli
70	128	97.0	1255	6	US-11-067-159-594	Sequence 594, App
71	128	97.0	1294	5	US-10-956-373-10	Sequence 10, Appli
72	124	93.9	23	6	US-11-009-533-50	Sequence 50, Appli
73	114	86.4	139	5	US-10-949-667-4	Sequence 4, Appli
74	114	86.4	634	3	US-09-854-356-8	Sequence 8, Appli
75	114	86.4	1256	3	US-09-854-356-2	Sequence 2, Appli
76	114	86.4	1256	3	US-09-854-356-14	Sequence 14, Appli
77	114	86.4	1257	5	US-10-484-067-2	Sequence 2, Appli
78	114	86.4	1260	3	US-09-870-759-118	Sequence 118, App
79	114	86.4	1260	3	US-09-751-708A-118	Sequence 118, App
80	114	86.4	1260	4	US-10-428-817A-114	Sequence 114, App
81	114	86.4	1260	5	US-10-937-758A-95	Sequence 95, Appli
82	114	86.4	1260	5	US-10-949-667-8	Sequence 8, Appli
83	71	53.8	15	3	US-09-354-533-56	Sequence 56, Appli
84	71	53.8	15	4	US-10-149-138-3929	Sequence 3929, Ap
85	71	53.8	15	4	US-10-149-138-4517	Sequence 4517, Ap
86	71	53.8	15	4	US-10-847-005-56	Sequence 56, Appli
87	71	53.8	15	4	US-10-149-138-3929	Sequence 3929, Ap
88	71	53.8	15	4	US-10-149-138-4517	Sequence 4517, Ap
89	71	53.8	15	6	US-11-121-347-56	Sequence 56, Appli
90	70	53.0	15	4	US-10-149-138-3891	Sequence 3891, Ap
91	70	53.0	15	4	US-10-149-138-4437	Sequence 4437, Ap
92	70	53.0	15	4	US-10-149-138-3891	Sequence 3891, Ap
93	70	53.0	15	4	US-10-149-138-4457	Sequence 4457, Ap
94	63	47.7	18	3	US-09-354-533-60	Sequence 60, Appli
95	63	47.7	18	4	US-10-245-871-578	Sequence 578, App
96	63	47.7	18	4	US-10-253-286-578	Sequence 578, App
97	63	47.7	18	4	US-10-647-005-60	Sequence 60, Appli
98	63	47.7	18	6	US-11-121-347-60	Sequence 60, Appli
99	55	41.7	11	4	US-10-149-138-2532	Sequence 2532, Ap
100	55	41.7	11	4	US-10-149-138-3237	Sequence 3237, Ap

ALIGNMENTS

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RESULT 1
US-10-956-373-26
; Sequence 26, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-373-26

Query Match          97.0%; Score 128; DB 5; Length 387;
Best Local Similarity 95.8%; Pred. No. 4.9e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
   |||||
Db 316 PLHNQEVTAEDGTQCEKCKSPCA 339

RESULT 2
US-10-302-663-2
; Sequence 2, Application US/10302663
; Publication No. US20040022785A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; TITLE OF INVENTION: EXPRESSION OF HERSTATIN, AN ALTERNATIVE HER-2/NEU PRODUCT, IN CEL
; TITLE OF INVENTION: EXPRESS EITHER P185HER-2 OR THE EGF RECEPTOR INHIBITS RECEPTOR A
; FILE REFERENCE: 49321-73
; CURRENT APPLICATION NUMBER: US/10/302,663
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 09/638,834
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 342
; OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 345
; OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 346
; OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
; FEATURE:
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; NAME/KEY: VARIANT
; LOCATION: 356
; OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 358
; OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 361
; OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence variant
; OTHER INFORMATION: position
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 376
; OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 394
; OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 404
; OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 413
; OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at this
US-10-302-663-2

Query Match          97.0%; Score 128; DB 4; Length 419;
Best Local Similarity 95.8%; Pred. No. 5.3e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
   |||||
Db 316 PLHNQEVTAEDGTQCEKCKSPCA 339

RESULT 3
US-10-344-470-2
; Sequence 2, Application US/10344470
; Publication No. US20040052796A1
; GENERAL INFORMATION:
; APPLICANT: Clinton, Gail M.
; TITLE OF INVENTION: EXPRESSION OF HERSTATIN, AN ALTERNATIVE TO HER-2/NEU PRODUCT, IN
; TITLE OF INVENTION: THAT EXPRESS EITHER P185HER-2 OR THE EGF RECEPTOR INHIBITS RECE
; TITLE OF INVENTION: CELL GROWTH
; FILE REFERENCE: 49321-81
; CURRENT APPLICATION NUMBER: US/10/344,470
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: PCT / US01/25502
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 09/638,834
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (342)..(342)
; OTHER INFORMATION: Applicants herein disclose Thr and Ser sequence variants at this
; OTHER INFORMATION: position
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (345)..(345)
; OTHER INFORMATION: Applicants herein disclose Leu and Pro sequence variants at this
; OTHER INFORMATION: position
; FEATURE:
; NAME/KEY: MISC_FEATURE
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LOCATION: (346)..(346)
OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (356)..(356)
OTHER INFORMATION: Applicants herein disclose Leu and Gln sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (358)..(358)
OTHER INFORMATION: Applicants herein disclose Met and Leu sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (361)..(361)
OTHER INFORMATION: Applicants herein disclose Gly, Asp, Ala and Val sequence variants
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (376)..(376)
OTHER INFORMATION: Applicants herein disclose Leu and Ile sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (394)..(394)
OTHER INFORMATION: Applicants herein disclose Pro and Arg sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (404)..(404)
OTHER INFORMATION: Applicants herein disclose Pro and Leu sequence variants at this
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (413)..(413)
OTHER INFORMATION: Applicants herein disclose Asp and Asn sequence variants at this
OTHER INFORMATION: position
US-10-344-470-2

Query Match 97.0%; Score 128; DB 4; Length 419;

Best Local Similarity 95.8%; Pred. No. 5.3e-10;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTORAEKCKSKPCA 24
|||||

Db 316 PLHNQEVTAEDGTORAEKCKSKPCA 339

RESULT 4

US-10-775-204-1811
Sequence 1811, Application US/10775204

Publication No. US20050186664A1

GENERAL INFORMATION:

APPLICANT: Rosen, Craig A.

APPLICANT: Haseltine, William A.

APPLICANT: Balance, David J.

APPLICANT: Turner, Andrew J.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF564

CURRENT APPLICATION NUMBER: US/10775,204

CURRENT FILING DATE: 2004-02-11

PRIOR FILING DATE: 2001-12-21

PRIOR APPLICATION NUMBER: 60/341,811

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/360,000

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: 60/378,950

PRIOR FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: 60/398,008

PRIOR FILING DATE: 2002-07-24

PRIOR APPLICATION NUMBER: 60/411,355

PRIOR FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/414,984

PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/417,611
PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 60/420,246
PRIOR FILING DATE: 2002-10-23
PRIOR APPLICATION NUMBER: 60/423,623
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/351,360
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2222
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1811
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-10-775-204-1811

Query Match 97.0%; Score 128; DB 5; Length 419;

Best Local Similarity 95.8%; Pred. No. 5.3e-10;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTORAEKCKSKPCA 24
|||||

Db 316 PLHNQEVTAEDGTORAEKCKSKPCA 339

RESULT 5

US-10-846-113A-9

Sequence 9, Application US/10846113A

Publication No. US2005023908A1

GENERAL INFORMATION:

APPLICANT: Shepard, H. Michael

APPLICANT: Clinton, Gail M.

APPLICANT: Lackey, David B.

APPLICANT: Jin, Pei

TITLE OF INVENTION: INTRON FUSION PROTEINS, AND

TITLE OF INVENTION: METHODS OF IDENTIFYING AND USING SAME

FILE REFERENCE: 17118-006001

CURRENT APPLICATION NUMBER: US/10/846,113A

CURRENT FILING DATE: 2004-05-14

PRIOR APPLICATION NUMBER: US 60/471,141

PRIOR FILING DATE: 2003-05-16

NUMBER OF SEQ ID NOS: 53

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 419

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Human ERBB2.c BUILD 31

US-10-846-113A-9

Query Match 97.0%; Score 128; DB 5; Length 419;

Best Local Similarity 95.8%; Pred. No. 5.3e-10;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTORAEKCKSKPCA 24
|||||

Db 316 PLHNQEVTAEDGTORAEKCKSKPCA 339

RESULT 6

US-10-485-683-2

Sequence 2, Application US/10485683

Publication No. US20040248196A1

GENERAL INFORMATION:

APPLICANT: ADAMS, TIMOTHY EDWARD

APPLICANT: BURGESS, ANTHONY WILKS

APPLICANT: ELLEMAN, THOMAS CHARLES

APPLICANT: GARRETT, THOMAS PETER JOHN

APPLICANT: JORISSEN, ROBERT NICHOLAS

APPLICANT: LOU, MEIZHEN

```
; APPLICANT: LOVRECEZ, GEORGE OSCAR
; APPLICANT: MCKERN, NEIL MORETON
; APPLICANT: NICE, EDOUARD COLLINS
; APPLICANT: WARD, COLIN WESLEY
; TITLE OF INVENTION: METHODS OF SCREENING BASED ON THE EGF RECEPTOR CRYSTAL
; TITLE OF INVENTION: STRUCTURE
; FILE REFERENCE: 051654/0104
; CURRENT APPLICATION NUMBER: US/10/485,683
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/AU02/01042
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: AU PR 6827
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: AU PR 6828
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/336,560
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 60/335,393
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: AU PS 2731
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/388,171
; PRIOR FILING DATE: 2002-06-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-485-683-2

Query Match          97.0%; Score 128; DB 5; Length 509;
Best Local Similarity 95.8%; Pred. No. 6.5e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRCCKSKPCA 24
|||||
Db 295 PLHNQEVTAEDGTQRCCKSKPCA 318
|||||

* RESULT 7
US-10-956-373-4
; Sequence 4, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; TITLE OF INVENTION: METHODS USING SAME
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 4
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-956-373-4

Query Match          97.0%; Score 128; DB 5; Length 575;
Best Local Similarity 95.8%; Pred. No. 7.5e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRCCKSKPCA 24
|||||
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Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339

RESULT 8
US-10-846-113A-7
; Sequence 7, Application US/10846113A
; Publication No. US20050239088A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, H. Michael
; APPLICANT: Clinton, Gail M.
; APPLICANT: Lackey, David B.
; APPLICANT: Jin, Pei
; TITLE OF INVENTION: INTRON FUSION PROTEINS, AND
; TITLE OF INVENTION: METHODS OF IDENTIFYING AND USING SAME
; FILE REFERENCE: 17118-006001
; CURRENT APPLICATION NUMBER: US/10/846,113A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/471,141
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human ERBB2.1.f
; US-10-846-113A-7

Query Match          97.0%; Score 128; DB 5; Length 575;
Best Local Similarity 95.8%; Pred. No. 7.5e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRCCKSKPCA 24
|||||
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339

RESULT 9
US-11-021-951-183
; Sequence 183, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHMIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; TITLE OF INVENTION: And Diagnostic Use Thereof
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003050
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 183
; LENGTH: 607
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-021-951-183

Query Match          97.0%; Score 128; DB 6; Length 607;
Best Local Similarity 95.8%; Pred. No. 7.9e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
    |||||
Db 294 PLHNQEVTAEDGTQRAEKCKSKPCA 317

RESULT 10
US-10-956-373-16
; Sequence 16, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-373-16

Query Match          97.0%; Score 128; DB 5; Length 614;
Best Local Similarity 95.8%; Pred. No. 8e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
    |||||
Db 316 PLHNQEVTAEDGTQRAEKCKSKPCA 339

RESULT 11
US-10-846-113A-6
; Sequence 6, Application US/10846113A
; Publication No. US2005023908A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, H. Michael
; APPLICANT: Clinton, Gail M.
; APPLICANT: Lackey, David B.
; APPLICANT: Jin, Pei
; TITLE OF INVENTION: INTRON FUSION PROTEINS, AND
; FILE REFERENCE: 17118-006001
; CURRENT APPLICATION NUMBER: US/10/846,113A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/471,141
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human ERBB2.1.e
US-10-846-113A-6
```

```
Query Match          97.0%; Score 128; DB 5; Length 633;
Best Local Similarity 95.8%; Pred. No. 8.3e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
    |||||
Db 316 PLHNQEVTAEDGTQRAEKCKSKPCA 339

RESULT 12
US-09-921-161-1
; Sequence 1, Application US/09921161
; Patent No. US20020090662A1
; GENERAL INFORMATION:
; APPLICANT: Ralph, Peter
; TITLE OF INVENTION: ANALYTICAL METHOD
; FILE REFERENCE: GENENT.066A
; CURRENT APPLICATION NUMBER: US/09/921,161
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/225,433
; PRIOR FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-921-161-1

Query Match          97.0%; Score 128; DB 3; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
    |||||
Db 316 PLHNQEVTAEDGTQRAEKCKSKPCA 339

RESULT 13
US-10-268-501-13
; Sequence 13, Application US/10268501
; Publication No. US20030086924A1
; GENERAL INFORMATION:
; APPLICANT: Slikowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: PI467R2P1
; CURRENT APPLICATION NUMBER: US/10/268,501
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 03/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 13
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-268-501-13

Query Match          97.0%; Score 128; DB 4; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
    |||||
Db 316 PLHNQEVTAEDGTQRAEKCKSKPCA 339

RESULT 14
US-10-608-626-13
; Sequence 13, Application US/10608626
; Publication No. US20040013667A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 13
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-608-626-13

Query Match          97.0%; Score 128; DB 4; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQCEKCKPCA 339

RESULT 15
US-10-719-310-13
; Sequence 13, Application US/10719310
; Publication No. US20040258685A1
; GENERAL INFORMATION:
; APPLICANT: Brunetta, Paul G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: THERAPY OF NON-MALIGNANT DISEASES OR DISORDERS WITH
; TITLE OF INVENTION: ANTI-ERBB2 ANTIBODIES
; FILE REFERENCE: P1979R1
; CURRENT APPLICATION NUMBER: US/10/719,310
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/428,027
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 13
; LENGTH: 645
; TYPE: PRT
; ORGANISM: human
US-10-719-310-13

Query Match          97.0%; Score 128; DB 5; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQCEKCKPCA 339

RESULT 16
US-11-044-749-13
; Sequence 13, Application US/11044749
; Publication No. US20050208043A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; TITLE OF INVENTION: Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/11/044,749
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US/09/602,812

; GENERAL INFORMATION:
; APPLICANT: Kelsey, Stephen M.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2P2
; CURRENT APPLICATION NUMBER: US/10/608,626
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US 10/268,501
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 13
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-044-749-13

Query Match          97.0%; Score 128; DB 6; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQCEKCKPCA 339

RESULT 17
US-11-154-465-13
; Sequence 13, Application US/11154465
; Publication No. US20050238640A1
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Sliwowski, Mark X.
; TITLE OF INVENTION: Humanized Anti-ErbB2 Antibodies and Treatment with
; TITLE OF INVENTION: Anti-ErbB2 Antibodies
; FILE REFERENCE: P1467R2
; CURRENT APPLICATION NUMBER: US/11/154,465
; CURRENT FILING DATE: 2005-06-16
; PRIOR APPLICATION NUMBER: US/09/602,812
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141,316
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 13
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-154-465-13

Query Match          97.0%; Score 128; DB 6; Length 645;
Best Local Similarity 95.8%; Pred. No. 8.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPCA 24
Db 316 PLHNQEVTAEDGTQCEKCKPCA 339

RESULT 18
US-09-854-356-3
; Sequence 3, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 653
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
US-09-854-356-3

```

Query Match 97.0%; Score 128; DB 3; Length 653;
Best Local Similarity 95.8%; Pred. No. 8.6e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCSPCA 24
|||
316 PLHNQEVTAEDGTORCEKCSPCA 339
Db

```

RESULT 19
US-10-956-373--2
; Sequence 2, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL E2Fb-2 POLYPEPTIDES AND KITS AND
; METHODS USING SAME

```

Query Match 97.0%; Score 128; DB 5; Length 678;
Best Local Similarity 95.8%; Pred. No. 8.9e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQVETAEDGTQRAEKCSPCA 24
316 PLHNOEVTAEDGTORCEKCSPCA 339
Dp

```

RESULT 20
US-10-846-113A-5
; Sequence 5, Application US/10846113A
; Publication No. US20050239088A1
; GENERAL INFORMATION:
; APPLICANT: Shepard, H. Michael
; APPLICANT: Clinton, Gail M.
; APPLICANT: Lackey, David B.
; APPLICANT: Jin, Pei
; TITLE OF INVENTION: INTRON FUSION PROTEINS, AND
; TITLE OF INVENTION: METHODS OF IDENTIFYING AND USING SAME
; FILE REFERENCE: 17118-006001
; CURRENT APPLICATION NUMBER: US/10/846,113A
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: US 60/471,141
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 680
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Human ERB2.1.d
US-10-846-113A-5

```

Query Match 97.0%; Score 128; DB 5; Length 680;
Best Local Similarity 95.8%; Pred. No. 8.9e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 318 PLHNQEVTAEDGTQRCCEKCCKPCA 341

```

RESULT 21
US-10-412-804A-4
; Sequence 4, Application US/10412804A
; Publication NO. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 685
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-412-804A-4

```

Query Match 97.0%; Score 128; DB 4; Length 685;
Best Local Similarity 95.8%; Pred. No. 9e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCKPCA 24
|||
Db 316 PLHNQEVTAEDGTORCEKCKPCA 339

```

RESULT 22
US-10-412-804A-11
; Sequence 11, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuguan
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412.804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-804A-11

```

Query Match 97.0%; Score 128; DB 4; Length 690;
Best Local Similarity 95.8%; Pred. No. 9.1e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCSPCA 24
|||
Db 316 PLHNOEVTAEDGTORCEKSPCA 339
|||

```
RESULT 23
US-09-854-356-7
; Sequence 7, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fusion protein
; OTHER INFORMATION: of ECD and delta PD of human HER-2/neu
US 09 854 356 7

Query Match          97.0%; Score 128; DB 3; Length 712;
Best Local Similarity 95.8%; Pred. No. 9.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTTORAEKCKSPCA 24
DB 316 PLHNOEVTADGTTORAEKCKSPCA 339

* RESULT 24
US-10-412-804A-10
; Sequence 10, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-804A-10

Query Match          97.0%; Score 128; DB 4; Length 715;
Best Local Similarity 95.8%; Pred. No. 9.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTTORAEKCKSPCA 24
DB 316 PLHNOEVTADGTTORAEKCKSPCA 339

RESULT 25
US-10-956-373-14
; Sequence 14, Application US/10956373
```

```
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Seia-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ErbB-2 POLYPEPTIDES AND KITS AND
; TITLE OF INVENTION: METHODS USING SAME
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-956-373-14

Query Match          97.0%; Score 128; DB 5; Length 717;
Best Local Similarity 95.8%; Pred. No. 9.5e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTTORAEKCKSPCA 24
DB 316 PLHNOEVTADGTTORAEKCKSPCA 339

RESULT 26
US-10-412-804A-6
; Sequence 6, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 720
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-412-804A-6

Query Match          97.0%; Score 128; DB 4; Length 720;
Best Local Similarity 95.8%; Pred. No. 9.5e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTTORAEKCKSPCA 24
DB 316 PLHNOEVTADGTTORAEKCKSPCA 339

RESULT 27
US-09-854-356-6
; Sequence 6, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheever, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
```

```
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 919
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:fusion protein
; OTHER INFORMATION: of ECD and PD of human HER-2/neu
US-09-854-356-6

Query Match          97.0%; Score 128; DB 3; Length 919;
Best Local Similarity 95.8%; Pred. No. 1.2e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

-QY 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339
|||||

* RESULT 28
US-10-775-204-1643
; Sequence 1643, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1643
; LENGTH: 1006
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-204-1643

Query Match          97.0%; Score 128; DB 5; Length 1006;
Best Local Similarity 95.8%; Pred. No. 1.4e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
Db 318 PLHNQEVTAEDGTQRCCKSKPCA 341
|||||

RESULT 29
US-10-146-473-72
; Sequence 72, Application US/10146473
; Publication No. US20030108888A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew
; APPLICANT: Gout, Ivan
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Gure, Ali
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146,473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 1253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-473-72

Query Match          97.0%; Score 128; DB 4; Length 1253;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339
|||||

RESULT 30
US-09-811-123-9
; Sequence 9, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Slikowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-Ecbb
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-811-123-9

Query Match          97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSKPCA 24
Db 316 PLHNQEVTAEDGTQRCCKSKPCA 339
|||||
```

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RESULT 31
US-09-811-115-3
; Sequence 3, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: King, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1255
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-811-115-3

Query Match      97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTQRAEKCSPCA 24
Db 316 PLHNOEVTADGTQRCCKSPCA 339

RESULT 32
US-09-765-973-2
; Sequence 2, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmermann, Susan
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; FILE REFERENCE: 210121.496
; CURRENT APPLICATION NUMBER: US/09/765,973
; CURRENT FILING DATE: 2001-01-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PR1
; ORGANISM: Homo sapien
US-09-765-973-2

Query Match      97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTQRAEKCSPCA 24
Db 316 PLHNOEVTADGTQRCCKSPCA 339

RESULT 33
US-09-354-533-68
; Sequence 68, Application US/09354533
; Publication No. US20020055614A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/354,533
; FILING DATE: 15-Jul-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C9
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 68:
US-09-354-533-68

Query Match      97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTQRAEKCSPCA 24
Db 316 PLHNOEVTADGTQRCCKSPCA 339

RESULT 34
US-09-769-508-2
; Sequence 2, Application US/09769508
; Patent No. US2002015527A1
; GENERAL INFORMATION:
; APPLICANT: STUART, SUSAN G.
; APPLICANT: MONAHAN, JOHN J.
; APPLICANT: LANGTON, BEATRICE CLAUDIA
; APPLICANT: HANCOCK, MIRIAM E.C.
; APPLICANT: CHAO, LORRINE A.
; APPLICANT: BLUFORD, PETER
; TITLE OF INVENTION: C-ERBB-2 EXTERNAL DOMAIN: GP75
; FILE REFERENCE: BBIO-111-C1
; CURRENT APPLICATION NUMBER: US/09/769,508
; CURRENT FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-769-508-2

Query Match      97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNOEVTADGTQRAEKCSPCA 24
Db 316 PLHNOEVTADGTQRCCKSPCA 339

RESULT 35
US-09-854-356-1
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; Sequence 1, Application US/09854356
; Patent No. US20020177567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Cheyssen, Dirk
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: SmithKline Beecham Biologicals S. A.
; FILE REFERENCE: 014058-009810PC
; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: DOMAIN
; LOCATION: (1)..(653)
; OTHER INFORMATION: extracellular domain (ECD)
; NAME/KEY: DOMAIN
; LOCATION: (676)..(1255)
; OTHER INFORMATION: intracellular domain (ICD)
; NAME/KEY: DOMAIN
; LOCATION: (990)..(1255)
; OTHER INFORMATION: phosphorylation domain (PD)
; NAME/KEY: DOMAIN
; LOCATION: (990)..(1048)
; OTHER INFORMATION: fragment of the phosphorylation domain, preferred
; OTHER INFORMATION: portion (delta PD)
; US-09-854-356-1

Query Match          97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCKSPCA 339

RESULT 36
US-09-930-125-2
; Sequence 2, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121-544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-930-125-2

Query Match          97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCKSPCA 339

RESULT 37
US-09-441-411-6
; Sequence 6, Application US/09441411
; Publication No. US20030008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-441-411-6

Query Match          97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCKSPCA 339

RESULT 38
US-09-984-092-4
; Sequence 4, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: F1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-984-092-4

Query Match          97.0%; Score 128; DB 3; Length 1255;
Best Local Similarity 95.8%; Pred. No. 1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
Db 316 PLHNQEVTAEDGTQRAEKCKSPCA 339

RESULT 39
US-10-207-655-45
; Sequence 45, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
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FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 45
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-45

Query Match 97.0%; Score 128; DB 4; Length 1255;
Best Local Similarity 95.8%; Pred.No.1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCSPCA 24
DB 316 PLHNQEVTAEDGTQRAEKCSPCA 339

RESULT 40
US-10-177-293-126
Sequence 126, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 126
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-126

Query Match 97.0%; Score 128; DB 4; Length 1255;
Best Local Similarity 95.8%; Pred.No.1.7e-09;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCSPCA 24

DB 316 PLHNQEVTAEDGTQRAEKCSPCA 339
Search completed: December 3, 2005, 08:08:27
JOB time : 122.455 secs

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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:48:55 ; Search time 7.09091 Seconds
(without alignments)
16.207 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHNQEVTAEDGTQRAEKCKPCA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	128	97.0	1255	7	US-11-022-562-213
2	80	60.6	17	7	US-11-060-646-8
3	39	29.5	52	6	US-10-846-172A-3
4	39	29.5	235	7	US-11-126-126-16
5	39	29.5	330	6	US-10-846-172A-7
6	39	29.5	333	6	US-10-846-172A-6
7	39	29.5	461	7	US-11-132-285-6
8	39	29.5	461	7	US-11-182-946-4
9	39	29.5	752	6	US-10-793-626-1036
10	38.5	29.2	154	6	US-10-467-657-158
11	38.5	29.2	154	6	US-10-467-657-6520
12	38.5	29.2	154	6	US-10-467-657-7634
13	37	28.0	160	6	US-10-467-657-5090
14	37	28.0	406	6	US-10-821-234-1026
15	37	28.0	425	6	US-10-793-626-110
16	37	28.0	425	6	US-10-821-234-1260
17	37	28.0	519	7	US-11-099-691-10
18	37	28.0	594	6	US-10-467-657-6376
19	36.5	27.7	658	6	US-10-467-657-4782
20	36.5	27.7	733	6	US-10-467-657-5858
21	36.5	27.7	915	6	US-10-131-826A-294
22	36.5	27.7	956	7	US-11-113-424-39
23	36	27.3	469	6	US-10-510-386-14
24	36	27.3	491	6	US-10-131-826A-278
25	36	27.3	697	7	US-11-074-176-214

Sequence 51, Appl
Sequence 18, Appl
Sequence 8624, Ap
Sequence 232, App
Sequence 180, App
Sequence 228, App
Sequence 1284, Ap
Sequence 26, Appl
Sequence 18, Appl
Sequence 32, Appl
Sequence 1387, Ap
Sequence 2040, Ap
Sequence 2, Appli
Sequence 90, Appl
Sequence 150, App
Sequence 164, App
Sequence 362, App
Sequence 1317, Ap
Sequence 1643, Ap
Sequence 24, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 73, Appl
Sequence 82, Appl
Sequence 1155, Ap
Sequence 650, App
Sequence 1716, Ap
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 53, Appl
Sequence 57, Appl
Sequence 124, App
Sequence 92, Appl
Sequence 2380, Ap
Sequence 21, Appl
Sequence 2, Appli
Sequence 128, App
Sequence 7682, Ap
Sequence 1500, Ap
Sequence 4, Appli
Sequence 1283, Ap
Sequence 9149, Ap
Sequence 378, App
Sequence 4586, Ap
Sequence 2624, Ap
Sequence 522, App
Sequence 2, Appli
Sequence 2482, Ap
Sequence 7, Appli
Sequence 1432, Ap
Sequence 5, Appli
Sequence 1744, Ap
Sequence 22, Appl
Sequence 357, App
Sequence 9, Appli
Sequence 2886, Ap
Sequence 3084, Ap
Sequence 52, Appl
Sequence 52, Appl
Sequence 208, App
Sequence 3562, Ap
Sequence 6462, Ap
Sequence 8396, Ap
Sequence 4, Appli
Sequence 8, Appli
Sequence 24, Appl
Sequence 79, Appl
Sequence 2140, Ap
Sequence 13, Appl
Sequence 2576, Ap
Sequence 1375, Ap

99 33 25.0 437 6 US-10-821-234-1549 Sequence 1549, Ap
100 33 25.0 445 6 US-10-467-657-3816 Sequence 3816, Ap

ALIGNMENTS

RESULT 1
US-11-022-562-213
; Sequence 213, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-562-213

Query Match 97.0%; Score 128; DB 7; Length 1255;
Best Local Similarity 95.8%; Pred. No. 8.8e-13;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPC 24
Db 316 PLHNQEVTAEDGTQRAEKCKPC 339

RESULT 2
US-11-060-646-8
; Sequence 8, Application US/11060646
; Publication No. US2005025555A1
; GENERAL INFORMATION:
; APPLICANT: Johns, Terrance Grant
; APPLICANT: Scott, Andrew Mark
; APPLICANT: Burgess, Anthony Wilks
; APPLICANT: Old, Lloyd J.
; APPLICANT: Adams, Timothy E.
; APPLICANT: Wittup, K. Dane
; APPLICANT: Chao, Ginger
; TITLE OF INVENTION: EGF Receptor Epitope Peptides and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 2332-1-011N
; CURRENT APPLICATION NUMBER: US/11/060,646
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: 60/546,602
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/584,623
; PRIOR FILING DATE: 2004-07-01
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: epitope peptide
US-11-060-646-8

Query Match 60.6%; Score 80; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQ 15
Db 2 PLHNQEVTAEDGTQ 16

RESULT 3
US-10-846-172A-3
; Sequence 3, Application US/10846172A
; Publication No. US20050257285A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; APPLICANT: Gupta, Goutam
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
; FILE REFERENCE: S-102.340
; CURRENT APPLICATION NUMBER: US/10/846,172A
; CURRENT FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Spinachia oleracea
US-10-846-172A-3

Query Match 29.5%; Score 39; DB 6; Length 52;
Best Local Similarity 58.3%; Pred. No. 3;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 GTQRAEKCKPC 23
Db 41 GTRRCMCKPC 52

RESULT 4
US-11-126-126-16
; Sequence 16, Application US/11126126
; Publication No. US20050250696A1
; GENERAL INFORMATION:
; APPLICANT: Fisher F., Eric
; APPLICANT: Edwards K., Carl
; APPLICANT: Kieft L., Gary
; TITLE OF INVENTION: Truncated Soluble Tumor Necrosis Factor Type-I and
; TITLE OF INVENTION: Type-II Receptors
; FILE REFERENCE: 02-006-A
; CURRENT APPLICATION NUMBER: US/11/126,126
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: 09/882,735
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/214,613
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: PCT/US97/12244
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: 60/039,792
; PRIOR FILING DATE: 1997-03-04
; PRIOR APPLICATION NUMBER: 60/039,314
; PRIOR FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: 60/037,737
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 60/032,534
; PRIOR FILING DATE: 1996-12-06
; PRIOR APPLICATION NUMBER: 60/021,443
; PRIOR FILING DATE: 1996-07-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-126-126-16

Query Match 29.5%; Score 39; DB 7; Length 235;

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Best Local Similarity 43.8%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 9 AEDGTQRAEKCSPCA 24
Db 128 ARPGTETSDVVCPC 143

RESULT 5
US-10-846-172A-7
; Sequence 7, Application US/10846172A
; Publication No. US20050257285A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
; FILE REFERENCE: S-102,340
; CURRENT APPLICATION NUMBER: US/10/846,172A
; CURRENT FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein
US-10-846-172A-7

Query Match 29.5%; Score 39; DB 6; Length 330;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 GTQRAEKCSPC 23
Db 319 GIRRRCMSKPC 330

RESULT 6
US-10-846-172A-6
; Sequence 6, Application US/10846172A
; Publication No. US20050257285A1
; GENERAL INFORMATION:
; APPLICANT: Los Alamos National Laboratory
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pierce's Disease
; FILE REFERENCE: S-102,340
; CURRENT APPLICATION NUMBER: US/10/846,172A
; CURRENT FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein
US-10-846-172A-6

Query Match 29.5%; Score 39; DB 6; Length 333;
Best Local Similarity 58.3%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 GTQRAEKCSPC 23
Db 322 GIRRRCMSKPC 333

RESULT 7
US-11-132-285-6
; Sequence 6, Application US/11132285
; Publication No. US20050244876A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR13 and TR14
; FILE REFERENCE: PF511P1
; CURRENT APPLICATION NUMBER: US/11/132,285
; CURRENT FILING DATE: 2005-05-19
; PRIOR APPLICATION NUMBER: US/10/046,433
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 60/261,960
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/618,570
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/144,087
; PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: 60/149,450
; PRIOR FILING DATE: 1999-07-18
; PRIOR APPLICATION NUMBER: 60/149,712
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/153,089
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-285-6

Query Match 29.5%; Score 39; DB 7; Length 461;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 9 AEDGTQRAEKCSPCA 24
Db 150 ARPGTETSDVVCPC 165

RESULT 8
US-11-182-946-4
; Sequence 4, Application US/11182946
; Publication No. US20050255100A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: Ni, Jian
; APPLICANT: Gentz, Reiner
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
; FILE REFERENCE: 1488.1280004
; CURRENT APPLICATION NUMBER: US/11/182,946
; CURRENT FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/186,643
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US/09/573,986
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-946-4

Query Match 29.5%; Score 39; DB 7; Length 461;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 9 AEDGTQRAEKCSPCA 24
Db 150 ARPGTETSDVVCPC 165

RESULT 9
US-10-793-626-1036
; Sequence 1036, Application US/10793626
```

```
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1036
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1036
```

```
Query Match          29.5%; Score 39; DB 6; Length 752;
Best Local Similarity 53.8%; Pred. No. 57;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 QEVTAEDGTQRAE 17
Db      709 KHVTAEDGKEKAK 721
```

```
RESULT 10
US-10-467-657-158
; Sequence 158, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 158
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-158
```

```
Query Match          29.2%; Score 38.5; DB 6; Length 154;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      6 EVTAEDGTQRAEKCCK 21
Db      138 KLVSEDTGTSR-EACTK 152
```

```
RESULT 11
US-10-467-657-6520
; Sequence 6520, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6520
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6520
```

```
Query Match          29.2%; Score 38.5; DB 6; Length 154;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      6 EVTAEDGTQRAEKCCK 21
Db      138 KLVSEDTGTSR-EACTK 152
```

```
RESULT 12
US-10-467-657-7634
; Sequence 7634, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7634
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7634
```

```
Query Match          29.2%; Score 38.5; DB 6; Length 154;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 8; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      6 EVTAEDGTQRAEKCCK 21
Db      138 KLVSEDTGTSR-EACTK 152
```

```
RESULT 13
US-10-467-657-5090
; Sequence 5090, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
```

; SEQ ID NO 5090
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5090

Query Match 28.0%; Score 37; DB 6; Length 160;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 5; Gaps 0;

Qy 13 TQRAEKCSPCA 24
|||:|
Db 134 THRRTCTAPCA 145

RESULT 14

US-10-821-234-1026
; Sequence 1026, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1026
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1026

Query Match 28.0%; Score 37; DB 6; Length 406;
Best Local Similarity 36.4%; Pred. No. 60;
Matches 4; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAED 11
|:|:|:|:|
Db 31 PIHNEDITYDE 41

RESULT 15

US-10-793-626-110
; Sequence 110, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 110
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-110

Query Match 28.0%; Score 37; DB 6; Length 425;
Best Local Similarity 42.1%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 0; Indels 8; Gaps 0;

Qy 2 LHNQEVTAEDGTORAEKCS 20
|||:|:|:|:|
Db 230 LHRGERSGEEVAQMERAS 248

RESULT 16

US-10-821-234-1260
; Sequence 1260, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1260
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1260

Query Match 28.0%; Score 37; DB 6; Length 425;
Best Local Similarity 46.2%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 HNOEVTAEDGTOR 15
||:|:|:|
Db 327 HNETILASSGTR 339

RESULT 17

US-11-099-691-10
; Sequence 10, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 1652936
US-11-099-691-10

Query Match 28.0%; Score 37; DB 7; Length 519;
Best Local Similarity 54.5%; Pred. No. 79;
Matches 6; Conservative 4; Mismatches 1; Indels 1; Gaps 0;

QY 1 PLHNQEVTAED 11
|:|:|:|:|:
DB 273 PVPNQDVTSD 283

RESULT 18
US-10-467-657-6376
; Sequence 6376, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6376
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6376

Query Match 28.0%; Score 37; DB 6; Length 594;
Best Local Similarity 41.2%; Pred. No. 91;
Matches 7; Conservative 2; Mismatches 8; Indels 8; Gaps 0;

QY 3 HNOEVTAEDGTQRAEKC 19
|:|:|:|:|:
DB 549 HHQPNQDDGEYAEKC 565

RESULT 19
US-10-467-657-4782
; Sequence 4782, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4782
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4782

Query Match 27.7%; Score 36.5; DB 6; Length 658;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 6; Indels 5; Gaps 1;

QY 3 HNOEVTAEDGTQRAEKCSPCA 24
|:|:|:|:|:
DB 120 HATQVKAEDG-----KLSSPTA 136

RESULT 20
US-10-467-657-5858
; Sequence 5858, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5858
; LENGTH: 733
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5858

Query Match 27.7%; Score 36.5; DB 6; Length 733;
Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 4 NOEVTA-EDGTQRAEK 18
|:|:|:|:|:
DB 485 NQDLTAVGHGTQVEE 500

RESULT 21
US-10-131-826A-294
; Sequence 294, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 294
; LENGTH: 915
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-294

Query Match 27.7%; Score 36.5; DB 6; Length 915;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Oy 7 VTAEDGTQRAEKCSK 21
Db 597 VLAEDG-RRCKKCTE 610
||||| :| :| :| :| :| :|

RESULT 22
US-11-113-424-39
; Sequence 39, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-113-424-39

Query Match 27.7%; Score 36.5; DB 7; Length 956;
Best Local Similarity 53.3%; Pred. No. 1.8e+02;
Matches 8; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

Oy 7 VTAEDGTQRAEKCSK 21
Db 638 VLAEDG-RRCKKCTE 651
||||| :| :| :| :| :| :|

RESULT 23
US-10-510-386-14

; Sequence 14, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294, 204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-14

Query Match 27.3%; Score 36; DB 6; Length 469;
Best Local Similarity 41.2%; Pred. No. 1e+02;
Matches 7; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Oy 6 EVTAEDGTQRAEKCSKP 22
Db 232 EITADIFTKKDEETGKP 248
||||| :| :| :| :| :| :|

RESULT 24
US-10-131-826A-278
; Sequence 278, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P33301C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352

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/ PRIOR FILING DATE: 1997-09-19
/ PRIOR APPLICATION NUMBER: 60/059588
/ PRIOR FILING DATE: 1997-09-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 550
/ SEQ ID NO 278
/ LENGTH: 491
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-131-826A-278

Query Match      27.3%; Score 36; DB 6; Length 491;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 AEDGTQRAEKS 20
Db 39 ATDGKEAKKA 50

RESULT 25
US-11-074-176-214
/ Sequence 214, Application US/11074176
/ Publication No. US20050250135A1
/ GENERAL INFORMATION:
/ APPLICANT: Klaenhammer, Todd R.
/ APPLICANT: Russell, William M.
/ APPLICANT: Altermann, Eric
/ APPLICANT: McAuliffe, Olivia
/ APPLICANT: Perill, Andrea Azcarate
/ TITLE OF INVENTION: Nucleic Acid Sequences Encoding
/ TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
/ FILE REFERENCE: 5051-694
/ CURRENT APPLICATION NUMBER: US/11/074,176
/ CURRENT FILING DATE: 2005-03-07
/ PRIOR APPLICATION NUMBER: 60/551,161
/ PRIOR FILING DATE: 2004-03-08
/ NUMBER OF SEQ ID NOS: 391
/ SOFTWARE: Fast-Seq for Windows Version 4.0
/ SEQ ID NO 214
/ LENGTH: 697
/ TYPE: PRT
/ ORGANISM: Lactobacillus acidophilus
US-11-074-176-214

Query Match      27.3%; Score 36; DB 7; Length 697;
Best Local Similarity 61.5%; Pred. No. 1.6e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 QEVTAEADGTQRAE 17
Db 430 QKLTEEDPTFRAE 442

RESULT 26
US-11-137-465-51
/ Sequence 51, Application US/11137465
/ Publication No. US2005025558A1
/ GENERAL INFORMATION:
/ APPLICANT: Agarwal, Pankaj
/ APPLICANT: Murdoch, Paul R.
/ APPLICANT: Rizvi, Safia, K.
/ APPLICANT: Smith, Randall, F.
/ APPLICANT: Xiang, Zhaoying
/ APPLICANT: Kabnick, Karen
/ TITLE OF INVENTION: NOVEL COMPOUNDS
/ FILE REFERENCE: GP50018
/ CURRENT APPLICATION NUMBER: US/11/137,465
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US/10/239,663
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: PCT/US01/09226
/ PRIOR FILING DATE: 2001-03-22
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/ PRIOR APPLICATION NUMBER: 60/192,158
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/192,668
/ PRIOR FILING DATE: 2000-03-27
/ PRIOR APPLICATION NUMBER: 60/200,166
/ PRIOR FILING DATE: 2000-04-27
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 51
/ LENGTH: 753
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-137-465-51

Query Match      27.3%; Score 36; DB 7; Length 753;
Best Local Similarity 47.1%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 4 NOEVTAEADGTQRAEKS 20
Db 698 NFEVAESDFTNNAMKCN 714

RESULT 27
US-11-078-735-18
/ Sequence 18, Application US/11078735
/ Publication No. US20050261477A1
/ GENERAL INFORMATION:
/ APPLICANT: CHAMPION, BRIAN ROBERT
/ APPLICANT: LENNARD, ANDREW CHRISTOPHER
/ APPLICANT: MCKENZIE, GRAHAME JAMES
/ APPLICANT: TUGAL, TAMARA
/ TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND MEDICAL TREATMENTS
/ TITLE OF INVENTION: COMPRISING NOTCH LIGAND PROTEINS
/ FILE REFERENCE: 674525-2019
/ CURRENT APPLICATION NUMBER: US/11/078,735
/ CURRENT FILING DATE: 2005-03-10
/ PRIOR APPLICATION NUMBER: PCT/GB03/03908
/ PRIOR FILING DATE: 2003-09-09
/ PRIOR APPLICATION NUMBER: PCT/GB03/03285
/ PRIOR FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: PCT/GB03/01525
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: GB 0300234.2
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: PCT/GB02/05137
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: PCT/GB02/05133
/ PRIOR FILING DATE: 2002-11-13
/ PRIOR APPLICATION NUMBER: GB 0220912.0
/ PRIOR FILING DATE: 2002-09-10
/ PRIOR APPLICATION NUMBER: GB 0220913.8
/ PRIOR FILING DATE: 2002-09-10
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 18
/ LENGTH: 618
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-078-735-18

Query Match      26.9%; Score 35.5; DB 7; Length 618;
Best Local Similarity 46.7%; Pred. No. 1.6e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 11 DGTQRAEKC-SKPCA 24
Db 425 DCRERADPCARPCA 439

RESULT 28
US-10-467-657-8624
/ Sequence 8624, Application US/10467657
```


; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8624
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8624

Query Match 26.5%; Score 35; DB 6; Length 26;
Best Local Similarity 50.0%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 10 EDGTQRAEKCSPC 23
Db 1 EDGEDADGRGSKPC 14

RESULT 29
US-10-793-626-252
; Sequence 252, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 252
; LENGTH: 164
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-252

Query Match 26.5%; Score 35; DB 6; Length 164;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NQEVTAEDG 12
Db 68 NEESAEDG 76

RESULT 30
US-10-485-517-180
; Sequence 180, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO

; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 180
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-180

Query Match 26.5%; Score 35; DB 6; Length 216;
Best Local Similarity 32.1%; Pred. No. 62;
Matches 9; Conservative 8; Mismatches 7; Indels 4; Gaps 2;

Qy 1 PLHNQEV-TAED--GTORAEKCSPCA 24
Db 147 PLNSVDINTKEDPKATIERSDSCAVPAA 174

RESULT 31
US-10-510-386-228
; Sequence 228, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 228
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-228

Query Match 26.5%; Score 35; DB 6; Length 229;
Best Local Similarity 43.8%; Pred. No. 66;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 6 EVTAEDGTQRAEKCCK 21
Db 66 ELKKDAGDQKAERTAK 81

RESULT 32
US-10-821-234-1284
; Sequence 1284, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1284
; LENGTH: 274

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1284

Query Match 26.5%; Score 35; DB 6; Length 274;
Best Local Similarity 33.3%; Pred. No. 80;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 4 NQEVTAEDGTQRAEKCSK 21

Db 48 SQEVTREDESTRSEEVTR 65

RESULT 33

US-10-131-826A-26

; Sequence 26, Application US/10131826A

; Publication No. US20050245730A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P330R1C128

; CURRENT APPLICATION NUMBER: US/10/131,826A

; CURRENT FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: 60/049911

; PRIOR FILING DATE: 1997-06-18

; PRIOR APPLICATION NUMBER: 60/056974

; PRIOR FILING DATE: 1997-08-26

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059117

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059122

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059184

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059352

; PRIOR FILING DATE: 1997-09-19

; PRIOR APPLICATION NUMBER: 60/059588

; PRIOR FILING DATE: 1997-09-19

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 26

; LENGTH: 296

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-131-826A-26

Query Match 26.5%; Score 35; DB 6; Length 296;
Best Local Similarity 46.2%; Pred. No. 88;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 HNOEVTAEEDGTQR 15

Db 116 HNYETTAKESLRR 128

RESULT 34

US-11-102-240-18

; Sequence 18, Application US/11102240

; Publication No. US20050260647A1

; GENERAL INFORMATION:

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRES

; TITLE OF INVENTION: ESOPHAGEAL TUMOR

; FILE REFERENCE: P3230R1C106C

; CURRENT APPLICATION NUMBER: US/11/102,240

; CURRENT FILING DATE: 2005-04-08

; PRIOR APPLICATION NUMBER: 10/063662

; PRIOR FILING DATE: 2002-05-07

; PRIOR APPLICATION NUMBER: 10/006867

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: PCT/US00/23328

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: 60/170262

; PRIOR FILING DATE: 199-12-09

; NUMBER OF SEQ ID NOS: 170

; SEQ ID NO 18

; LENGTH: 301

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-102-240-18

Query Match 26.5%; Score 35; DB 7; Length 301;

Best Local Similarity 43.8%; Pred. No. 89;

Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 7 VTAEDGTQRAEKCSK 22

Db 115 LTAIEGTAHGEPCHFP 130

RESULT 35

US-11-074-176-32

; Sequence 32, Application US/11074176

; Publication No. US20050250135A1

; GENERAL INFORMATION:

; APPLICANT: Klaenhammer, Todd R.

; APPLICANT: Russell, William M.

; APPLICANT: Altermann, Eric

; APPLICANT: McAuliffe, Olivia

; APPLICANT: Perill, Andrea Azcarate

; TITLE OF INVENTION: Nucleic Acid Sequences Encoding

; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore

; FILE REFERENCE: 5051-694

; CURRENT APPLICATION NUMBER: US/11/074,176

; CURRENT FILING DATE: 2005-03-07

; PRIOR APPLICATION NUMBER: 60/551,161

; PRIOR FILING DATE: 2004-03-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 32

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Lactobacillus acidophilus

US-11-074-176-32

Query Match 26.5%; Score 35; DB 7; Length 333;
Best Local Similarity 43.8%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 LHNQEVTAEDGTQRAE 17


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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 90
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-90
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Query Match          26.5%; Score 35; DB 6; Length 468;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 LHNQEVTAE 10
Db      31 LHNRELSAE 39
```

```
RESULT 40
US-11-102-240-150
; Sequence 150, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
; FILE REFERENCE: P323OR1C106C
; CURRENT APPLICATION NUMBER: US/11/102,240
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: 10/063662
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 199-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 150
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-102-240-150
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Query Match          26.5%; Score 35; DB 7; Length 468;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      2 LHNQEVTAE 10
Db      31 LHNRELSAE 39
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Search completed: December 3, 2005, 08:04:41
Job time : 8.09091 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:36:13 ; Search time 25.0909 Seconds
(without alignment)
92.033 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHNQEVTAEDGTQRAEKSKPCA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_80.*

1: Piri1.*

2: Piri2.*

3: Piri3.*

4: Piri4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB ID	Description
1	128	97.0	1255	1	A24571	protein-tyrosine k
2	114	86.4	1260	1	TVRTNU	protein-tyrosine k
3	113	85.6	1254	2	I48161	p-185 precursor -
4	50	37.9	686	2	A34612	zinc finger protei
5	49	37.1	1210	1	GQHUE	epidermal growth f
6	48	36.4	214	2	H90840	hypothetical prote
7	48	36.4	214	2	G85698	hypothetical prote
8	48	36.4	644	2	A36325	epidermal growth f
9	48	36.4	644	2	B71409	hypothetical prote
10	48	36.4	1210	2	A53183	epidermal growth f
11	48	36.4	1224	2	T19749	hypothetical prote
12	47	35.6	774	2	T00488	hypothetical prote
13	46	34.8	286	2	T05061	hypothetical prote
14	46	34.8	651	2	UC7705	death receptor-6 -
15	46	34.8	1390	2	T30346	insulin receptor -
16	46	34.8	2647	2	T28161	hypothetical prote
17	45	34.1	196	2	T49548	hypothetical prote
18	45	34.1	379	2	C84577	probable nucleosom
19	45	34.1	620	2	JU0273	hemagglutinin - me
20	45	34.1	742	2	E84285	hypothetical prote
21	45	34.1	873	2	H96503	protein F9C16.17 l
22	44.5	33.7	499	2	S70113	hypothetical prote
23	44	33.3	91	2	E81715	ferredoxin [2Fe-2S
24	44	33.3	268	2	AE3311	cytochrome c1 fimp
25	44	33.3	288	2	PH1917	FL-160-1 protein -
26	44	33.3	577	2	T09024	proline-rich prote
27	44	33.3	609	2	T40625	single-stranded DN
28	44	33.3	717	2	T04434	replication protei
29	44	33.3	1051	2	C95367	conserved hypothet

30	44	33.3	1422	2	T42636	protein-tyrosine-p
31	43.5	33.0	606	1	W1WLB5	E1 protein - human
32	43.5	33.0	681	2	I52603	MPS1 protein - mou
33	43.5	33.0	707	2	S60588	drebrin A - rat
34	43	32.6	91	2	G71562	ferredoxin [2Fe-2S
35	43	32.6	199	1	I39734	CBS domain-contain
36	43	32.6	204	2	AC1902	hypothetical prote
37	43	32.6	296	2	T20005	hypothetical prote
38	43	32.6	450	2	JC7266	3',5'-cyclic-nucle
39	43	32.6	516	2	S28060	serum response fac
40	43	32.6	585	2	JC6556	Y chromosome sex-d
41	43	32.6	655	2	T34219	hypothetical prote
42	43	32.6	701	2	T17243	hypothetical prote
43	43	32.6	1039	2	S46347	pol polyprotein -
44	43	32.6	1101	2	T16840	hypothetical prote
45	43	32.6	1293	2	B40025	maleless protein,
46	43	32.6	2185	1	S60200	acetyl-CoA carboxy
47	43	32.6	2396	2	T13714	kakapo gene protei
48	43	32.6	3343	2	S44887	ZK112.7 protein -
49	43	32.6	5138	2	B96695	hypothetical prote
50	42.5	32.2	275	2	S21348	probable pol polyp
51	42	31.8	77	1	XKTO	metallocarboxypept
52	42	31.8	163	2	A97609	crea protein limpo
53	42	31.8	163	2	AE2831	conserved hypothet
54	42	31.8	215	2	A60166	hemiferrin - bovin
55	42	31.8	216	1	A39684	hemiferrin - rat
56	42	31.8	222	2	F95367	hypothetical prote
57	42	31.8	284	2	T40927	hypothetical wfil
58	42	31.8	297	2	S51278	alternative respir
59	42	31.8	353	2	T04094	ubiquinol-cytochro
60	42	31.8	450	1	C29413	prolyl-tRNA synthe
61	42	31.8	499	2	D75416	uroconase (urocana
62	42	31.8	559	2	G83897	hypothetical prote
63	42	31.8	603	2	S76615	hypothetical prote
64	42	31.8	687	2	T30958	hypothetical prote
65	42	31.8	1082	2	T05075	hypothetical prote
66	42	31.8	1125	2	B41206	microtubule-associ
67	42	31.8	1941	2	T23979	hypothetical prote
68	42	31.8	1943	2	T23986	hypothetical prote
69	41.5	31.4	273	2	T01985	zinc-finger protei
70	41.5	31.4	328	2	AI0226	N-acetyluramoyl-L
71	41	31.1	194	2	JS0664	interferon precurs
72	41	31.1	201	2	S44540	DNA-directed DNA p
73	41	31.1	240	2	H81420	probable iron-bind
74	41	31.1	365	2	T25917	hypothetical prote
75	41	31.1	453	2	S59401	hypothetical prote
76	41	31.1	520	2	T34383	hypothetical prote
77	41	31.1	550	2	A11522	flagellar basal-bo
78	41	31.1	594	2	S74576	probable flavoprot
79	41	31.1	617	2	D86248	protein T23J18.15
80	41	31.1	704	2	A34337	propionyl-CoA carb
81	41	31.1	843	2	S44868	kinesin heavy chai
82	41	31.1	958	2	T20621	hypothetical prote
83	41	31.1	975	1	A31497	kinesin heavy chai
84	41	31.1	1002	2	T09438	ToxR-activated lip
85	41	31.1	1013	2	B82276	ToxR-activated gen
86	41	31.1	1030	2	T18374	B-cell receptor pr
87	41	31.1	1172	2	F96503	protein F9C16.13 l
88	41	31.1	1536	1	RGBYS3	regulatory protein
89	41	31.1	1599	2	T15854	hypothetical prote
90	41	31.1	1984	2	T13171	probable vitellogen
91	40.5	30.7	171	2	F72578	hypothetical prote
92	40.5	30.7	224	2	T06736	GTP-binding protei
93	40.5	30.7	403	1	G70311	histidine-tRNA lig
94	40.5	30.7	621	1	S20145	replication factor
95	40	30.3	129	2	S44751	C0664.4 protein -
96	40	30.3	144	2	A39499	6-pyruvoyltetrahyd
97	40	30.3	156	2	I40704	gene eae ORF4 homo
98	40	30.3	156	2	D86045	hypothetical prote
99	40	30.3	156	2	H91198	Cest protein limpo
100	40	30.3	156	2	I41196	Tir chaperone - Es

ALIGNMENTS

RESULT 1

A24571
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N;Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB
C;Species: Homo sapiens (man)
C;Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C;Accession: A24571; A25491; A44188; B44188; 159509; I57622
R;Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A;Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth factor
A;Reference number: A24571; MUID:86118663; PMID:3003577
A;Accession: A24571
A;Molecule type: mRNA
A;Residues: 1-1255 <YAM>
A;Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:g31197; PIDN:C
R;Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A;Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epidermal
A;Reference number: A25491; MUID:86016729; PMID:2995967
A;Accession: A25491
A;Molecule type: DNA
A;Residues: 737-1031 <SEM>
A;Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:
R;Coussens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P.
Science 230, 1132-1139, 1985
A;Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromo-
A;Reference number: A44188; MUID:86070181; PMID:2999974
A;Accession: A44188
A;Molecule type: DNA
A;Residues: 740-910 <COUL>
A;Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:
A;Accession: B44188
A;Molecule type: mRNA
A;Residues: 1-517, 'RALL', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A;Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986
R;King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A;Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A;Reference number: I59509; MUID:85272597; PMID:2992089
A;Accession: I59509
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 832-909 <REX>
A;Cross-references: UNIPARC:UPI0000070A3F; GB:I29395; NID:g459807; PIDN:AAA35809.1; PID:
R;Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A;Title: Human HSR2 (neu) promoter: evidence for multiple mechanisms for transcriptional
A;Reference number: I57622; MUID:87286898; PMID:3039351
A;Accession: I57622
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-191 <TAL>
A;Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:
C;Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
C;Genetics:
A;Gene: GDB:ERRB2; NCL; NEU; HER-2
A;Cross-references: GDB:I20613; OMIM:164870
A;Map position: 17q21.1-17q21.1
A;Map position: 25/1; 75/3; 147/1; 883/3
A;Note: the list of introns is incomplete
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho-
inase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
F;22-653/Domain: extracellular #status predicted <EXT>
F;70-304/Domain: EGF receptor extracellular domain repeat <BE1>
F;395-605/Domain: EGF receptor extracellular domain repeat <EE2>

F;654-675/Domain: transmembrane #status predicted <TMM>
F;676-1255/Domain: intracellular #status predicted <INT>
F;718-983/Domain: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif

F;68,124,187,259,530,571,629/Binding site: carbohydrate (Asn) (covalent) #status predic
F;686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F;753/Active site: Lys #status predicted
F;1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. No. 6.7e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPKCA 24

|||||
Db 316 PLHNQEVTAEDGTQRCCKCKPKCA 339

RESULT 2

TVRTNU
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C;Accession: A24562; A61204
R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A;Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A;Reference number: A24562; MUID:86118662; PMID:3945311
A;Accession: A24562
A;Molecule type: mRNA
A;Residues: 1-1260 <BAR>
A;Cross-references: UNIPROT:P06494; UNIPARC:UPI0000161B83; EMBL:X03362; NID:g56745; PID:
R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
Carcinogenesis 12, 1975-1978, 1991
A;Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no

2-thiazolylformamide or N-methyl-N-nitrosourea.

A;Reference number: A61204; MUID:92035293; PMID:1682063

A;Accession: A61204

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 637-663, 'V', 665-702 <MAS>

A;Cross-references: UNIPARC:UPI00001725C8

A;Note: authors translated the codon GCA for residue 25 as Val

C;Genetics:

A;Gene: neu

C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosph
F;1-13/Domain: signal sequence #status predicted <SIG>
F;20-1260/Product: protein-tyrosine kinase neu #status predicted <MAT>
F;658-680/Domain: transmembrane #status predicted <TMM>
F;723-988/Domain: protein kinase homology <KIN>
F;731-739/Region: protein kinase ATP-binding motif
F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;691/Binding site: phosphate (Thr) (covalent) #status predicted
F;758/Active site: Lys #status predicted
F;882,1227,1253/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 86.4%; Score 114; DB 1; Length 1260;
Best Local Similarity 87.5%; Pred. No. 8.4e-09;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCKPKCA 24

|||||
Db 320 PLHNQEVTAEDGTQRCCKCKPKCA 343

RESULT 3

I48161
p-185 precursor - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C;Accession: I48161
R;Nakamura, T.; Ushijima, T.; Ishizaka, Y.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa

Gene 140, 251-255, 1994
A;Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A;Reference number: I48161; MUID:94193007; PMID:7908275
A;Accession: I48161
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1254 <RES>
A;Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:g493236; PIDN:
C;Genetics:
A;Gene: neu
C;Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C;Keywords: Dmp
F;718-983/Region: protein kinase homology <KIN>
F;726-734/Region: protein kinase ATP-binding motif

Query Match 85.6%; Score 113; DB 2; Length 1254;
Best Local Similarity 87.5%; Pred. No. 1.2e-08;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCCKPCA 24
Db 316 PLNNQEVTAEDGTQCEKCKSKCA 339
||:|||||
||:|||||

RESULT 4
A34612
zinc finger protein ZNF7 - human
N;Alternate names: zinc finger protein kox4
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34612; A56409; S10421; I37972
R;Lania, L.; Dotti, E.; Pannuti, A.; Pascucci, A.; Pengue, G.; Feliciello, I.; La Mantia
Genomics 6, 333-340, 1990
A;Title: cDNA isolation, expression analysis, and chromosomal localization of two human
A;Reference number: A34612; MUID:90169993; PMID:2106481
A;Accession: A34612
A;Molecule type: mRNA
A;Residues: 1-686 <LAN>
A;Cross-references: UNIPROT:P17097; UNIPARC:UPI000013C3F8; GB:M29580; NID:g340445; PIDN:
R;Bray, P.; Lichter, P.; Thiesen, H.J.; Ward, D.C.; David, I.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 9563-9567, 1991
A;Title: Characterization and mapping of human genes encoding zinc finger proteins.
A;Reference number: A56409; MUID:92052132; PMID:1946370
A;Accession: A56409
A;Molecule type: DNA
A;Residues: 425-589 <BRA>
A;Cross-references: UNIPARC:UPI0000178A54; GB:M77170
R;Thiesen, H.J.
submitted to the EMBL Data Library, March 1990
A;Reference number: S10397
A;Accession: S10421
A;Molecule type: mRNA
A;Residues: 413-468 <THI>
A;Cross-references: UNIPARC:UPI000016ABC5; EMBL:X52335; NID:g34165; PIDN:CAA36561.1; PID
R;Thiesen, H.J.
New Biol. 2, 363-374, 1990
A;Title: Multiple genes encoding zinc finger domains are expressed in human T cells.
A;Reference number: I37949; MUID:91145339; PMID:2288909
A;Accession: I37972
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 413-468 <RES>
A;Cross-references: UNIPARC:UPI000016ABC5; EMBL:X52335; NID:g34165; PIDN:CAA36561.1; PID
C;Genetics:
A;Gene: GDB:ZNF7
A;Cross-references: GDB:120509; OMIM:194531
A;Map position: 8q24.3-8q24.3
C;Superfamily: zinc finger protein ZFP-36; LIM metal-binding repeat homology
C;Keywords: DNA binding; zinc finger

Query Match 37.9%; Score 50; DB 2; Length 686;
Best Local Similarity 47.6%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 PLHNQEVTAEDGTQRAEKCCK 21
Db 183 PLESQGESAGMSQRCCECGK 203
||:|||||
||:|||||

RESULT 5
QOHUE
epidermal growth factor receptor precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 27-Nov-1985 #text_change 05-Oct-2004
C;Accession: A00641; A25772; S30024; A38672; A43615; A23062; A05281; A60143; A
R;Ullrich, A.; Coussens, L.; Hayflick, J.S.; Dull, T.J.; Gray, A.; Tam, A.W.; Lee, J.;
rg, P.H.
Nature 309, 418-425, 1984
A;Title: Human epidermal growth factor receptor cDNA sequence and aberrant expression o
A;Reference number: A00641; MUID:84219729; PMID:6328312
A;Accession: A00641
A;Molecule type: mRNA
A;Residues: 1-1210 <ULL>
A;Cross-references: UNIPROT:P00533; UNIPARC:UPI0000050F30; EMBL:X00588; NID:g31113; PID
A;Note: the authors translated the codon AAG for residue 540 as Asn
R;Ishii, S.; Xu, Y.; Stratton, R.H.; Roe, B.A.; Merlino, G.T.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 82, 4920-4924, 1985
A;Title: Characterization and sequence of the promoter region of the human epidermal gr
A;Reference number: A25772; MUID:85270438; PMID:2991899
A;Accession: A25772
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <ISH>
A;Cross-references: UNIPARC:UPI000016A882; GB:M11234; NID:g181981; PIDN:AAA52370.1; PID
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ullrich, A.; Waterfield, M.
Oncogene Res. 1, 375-396, 1987
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification
A;Reference number: S30024; MUID:88217333; PMID:3329716
A;Accession: S30024
A;Molecule type: DNA
A;Residues: 1-29 <HA2>
A;Cross-references: UNIPARC:UPI000016A882; EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID
R;Haley, J.D.; Waterfield, M.D.
J. Biol. Chem. 266, 1746-1753, 1991
A;Title: Contributory effects of de Novo transcription and premature transcript termina
A;Reference number: A38672; MUID:91107677; PMID:1988448
A;Accession: A38672
A;Molecule type: DNA
A;Residues: 1-29 <HAL>
A;Cross-references: UNIPARC:UPI000016A882; GB:M38425; NID:g181977; PIDN:AAA63171.1; PID
A;Experimental source: carcinoma cell line A431-7
R;Xu, Y.; Ishii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Me
Nature 309, 806-810, 1984
A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs
A;Reference number: A00642; MUID:84245835; PMID:6330563
A;Accession: A00642
A;Molecule type: mRNA
A;Residues: 'RCAWRRA' 150-187, 'KSVIOAV' 195, 'W', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-32
' 798-799, 'TD', 802-811, 'R', 813-942 <XUY>
A;Cross-references: UNIPARC:UPI00001725BD
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF rece
R;Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I
Science 224, 843-848, 1984
A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplification
A;Reference number: A43615; MUID:84196372; PMID:6326261
A;Accession: A43615
A;Molecule type: mRNA
A;Residues: 713-964 <LIN>
A;Cross-references: UNIPARC:UPI00001725BE
A;Experimental source: epidermoid carcinoma cell line A431
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.
Biochem. Biophys. Res. Commun. 124, 125-132, 1984
A;Reference number: A23062; MUID:85046483; PMID:6093780
A;Accession: A23062
A;Molecule type: mRNA

A:Description: A novel protein from carrot embryo.

A:Reference number: T14284

A:Accession: T00488

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: mRNA

A:Residues: 1-774 <XUZ>

A:Cross-references: UNIPROT:O80379; UNIPARC:UPT00000A89BA; EMBL:AB012704; NID:G3551248;

A:Experimental source: embryogenic callus

C:Genetics:

A:Note: 184-1d10

Query Match 35.6%; Score 47; DB 2; Length 774;
Best Local Similarity 40.0%; Pred. No. 56;

Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 4 NQEVTAEDGTQRAEKCKPC 23

DB 313 NEEITQDESTRAKSPKLC 332

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||:|:|:|:|:|:|:|:|:|

RESULT 13

T05061

hypothetical protein M3E9.140 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T05061

R:Bevan, M.; Vandenbol, M.; Jallet, C.; Portetelle, D.; Hoheisel, J.; Mewes, H.W.; Mayer

submitted to the Protein Sequence Database, March 1999

A:Reference number: Z15396

A:Accession: T05061

A:Molecule type: DNA

A:Residues: 1 286 <BEV>

A:Cross-references: UNIPROT:O65591; UNIPARC:UPI00000A63D0; EMBL:AL022223

A:Experimental source: cultivar Columbia; BAC clone M3E9

C:Genetics:

A:Map position: 4

A:Introns: 100/1; 129/3; 161/1; 181/3; 208/1; 241/3; 260/2

A:Note: M3E9.140

Query Match 34.8%; Score 46; DB 2; Length 286;
Best Local Similarity 38.1%; Pred. No. 30;

Matches 8; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 3 HNQEVTAEDGTQRAEKCKPC 23

DB 192 HVAHLKPSDGGSAATQCDKPC 212

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||:|:|:|:|:|:|:|:|:|

RESULT 14

JC7705

death receptor-6 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004

C:Accession: JC7705

R:Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A:Reference number: JC7705; MUID:21308433; PMID:11414698

A:Accession: JC7705

A:Molecule type: mRNA

A:Residues: 1-651 <BRI>

A:Cross-references: UNIPROT:Q98SM6; UNIPARC:UPI000017CBA0; GB:AF349908

C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs

to the TNF receptor superfamily, and is involved in cell death and/or survival signaling cascade.

C:Genetics:

A:Gene: dr-6

C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

C:Keywords: ovary

F:1-21/Domain: signal sequence #status predicted <SIG>

F:52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <EC1>

F:332-350/Domain: transmembrane #status predicted <TM>

F:410-475/Domain: death domain #status predicted <DE0>

F:551-651/Region: conserved cytoplasmic #status predicted

Query Match 34.8%; Score 46; DB 2; Length 651;
Best Local Similarity 50.0%; Pred. No. 67;

Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 10 EDGTQRAEKCKPC 23

DB 85 ENGIERCHPCRKPC 98

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||:|:|:|:|:|:|:|:|:|

RESULT 15

T30346

insulin receptor - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C:Accession: T30346

R:Graf, R.; Neuenschwander, S.; Brown, M.R.; Ackermann, U.

Insect Mol. Biol. 6, 151-163, 1996

A:Title: Insulin mediated secretion of ecdysteroids from mosquito ovaries and molecular

A:Reference number: Z20834

A:Accession: T30346

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: mRNA

A:Residues: 1-1390 <GRA>

A:Cross-references: UNIPROT:Q93105; UNIPARC:UPI000012D6AB; EMBL:U72939; NID:gl620749; P

C:Superfamily: insulin receptor; protein kinase homology

Query Match 34.8%; Score 46; DB 2; Length 1390;

Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 15 RAEKCKPC 24

DB 1048 RGEKCNQPCA 1057

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||:|:|:|:|:|:|:|:|:|

RESULT 16

T28161

hypothetical protein FCR3-varT11-1 - malaria parasite (Plasmodium falciparum) (fragment

C:Species: Plasmodium falciparum

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T28161

R:Hernandez-Rivas, R.; Mattei, D.; Sterkers, Y.; Peterson, D.S.; Wellem, T.E.; Scherf,

Mol. Cell. Biol. 17, 604-611, 1997

A:Title: Expressed var genes are found in Plasmodium falciparum subtelomeric regions.

A:Reference number: Z20483; MUID:97154495; PMID:9001213

A:Accession: T28161

A:Status: preliminary; translated from GB/EMBL/DBSJ

A:Molecule type: DNA

A:Residues: 1-2647 <HER>

A:Cross-references: UNIPROT:P90580; UNIPARC:UPI0000083525; EMBL:U67959; NID:gl794255; P

A:Experimental source: strain FCQ27/PNG

C:Genetics:

A:Introns: 2158/3

A:Note: FCR3-varT11-1

Query Match 34.8%; Score 46; DB 2; Length 2647;
Best Local Similarity 47.6%; Pred. No. 2.6e+02;

Matches 10; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 LHNQEVTAEDGTQRAEKCKSP 22

DB 727 LSDSEDEEDIPQRQNKCAK 747

||:|:|:|:|:|:|:|:|:|

||:|:|:|:|:|:|:|:|:|

RESULT 17

T49548

hypothetical protein B21J21.260 [imported] - Neurospora crassa

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C:Accession: T49548

R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,

submitted to the Protein Sequence database, May 2000

A:Reference number: 225022

A:Accession: T49548

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-196 <SCH>

A:Cross-references: UNIPARC:UPI0000179D39; EMBL:AL355929; GSPDB:GN00116; NCSP:B21J21.260

A:Experimental source: BAC clone B21J21; strain OR74A

C:Genetics:

A:Gene: NCSP:B21J21.260

A:Map position: 6

C:Superfamily: Neurospora crassa hypothetical protein B21J21.260

Query Match

Best Local Similarity 34.1%; Score 45; DB 2; Length 196;

Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Oy 1 PLHNQEVTAEDGTQRAEKCS 20

|||||:|:|:|

Db 155 PLHQRLTLDAGSQPKNCA 174

RESULT 18

C84577

Probable nucleosome assembly protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: C84577

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.

euss, D.; Nietman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84577

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-379 <STO>

A:Cross-references: UNIPROT:Q9ZUP3; UNIPARC:UPI00000AC55A; GB:AE002093; NID:g4191778; PI

C:Genetics:

A:Gene: At2g19480

A:Map position: 2

Query Match

Best Local Similarity 34.1%; Score 45; DB 2; Length 379;

Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Oy 2 LHNQEVTAEDGTQRAEKCSK 21

|||||:|:|:|

Db 134 LKNEITAEETERDEGALK 153

RESULT 19

JU0273

hemagglutinin - measles virus

C:Species: measles virus

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JU0273

R:Komase, K.; Hago, T.; Yoshikawa, Y.; Sato, T.A.; Yamanouchi, K.

Virus Genes 4, 163-172, 1990

A:Title: Molecular analysis of structural protein genes of the Yamagata-1 strain of defe

A:Reference number: JU0273; MUID:90385701; PMID:2402882

A:Accession: JU0273

A:Molecule type: mRNA

A:Residues: 1-620 <KOM>

A:Cross-references: UNIPROT:P28081; UNIPARC:UPI0000178694

A:Experimental source: strain Yamagata-1

C:Genetics:

A:Gene: H

C:Superfamily: measles virus hemagglutinin

C:Keywords: Glycoprotein; transmembrane protein

F:35-58/Domain: transmembrane #status predicted <TMM>

F:168,187,200,215,238/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 34.1%; Score 45; DB 2; Length 620;

Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 VTAEDGTQRAEKC 19

|||||:|:|:|

Db 608 VTREDGTNRQSC 620

RESULT 20

E84285

hypothetical protein Vng1303c [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C:Accession: E84285

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,

Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L

A:Title: Genome sequence of Halobacterium species NRC-1.

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: E84285

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-742 <STO>

A:Cross-references: UNIPROT:Q9HQ68; UNIPARC:UPI000006385E; GB:AE004437; NID:gl0580823;

C:Genetics:

A:Gene: VNG1303C

C:Superfamily: conserved hypothetical protein yyaL

Query Match

Best Local Similarity 34.1%; Score 45; DB 2; Length 742;

Matches 9; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Oy 1 PLHNQEVTAEDGTQRAEKSKPCA 24

|||||:|:|:|

Db 701 PLWAGRTGGDGTGRAYVCCRACS 724

RESULT 21

H96503

protein F9C16.17 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: H96503

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: H96503

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-873 <STO>

A:Cross-references: UNIPROT:Q9LP01; UNIPARC:UPI00000AB3E6; GB:AE005173; NID:g8778675; P

C:Genetics:

A:Gene: F9C16.17

A:Map position: 1

Query Match

Best Local Similarity 34.1%; Score 45; DB 2; Length 873;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Oy 5 QEYTAEDGTQRAEKCS 20

:|:|:|:|:|

Db 83 ESWVADNVVTEKCN 98

RESULT 22

S70113

hypothetical protein YDR348c - yeast (*Saccharomyces cerevisiae*)

A:Alternative names: hypothetical protein D9651.1f

C:Species: *Saccharomyces cerevisiae*

C:Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C:Accession: S70113

R;Du, Z.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of *S. cerevisiae* cosmid 9651.

A:Reference number: S70098

A:Accession: S70113

A:Molecule type: DNA

A:Residues: 1-499 <DUZ>

A:Cross-references: UNIPROT:Q05518; UNIPARC:UPI0000053247; EMBL:U51032; NID:gl230659; PI

C:Genetics:

A:Gene: MIPS:YDR348C

A:Cross-references: SGD:S0002756

A:Map position: 4R

C:Superfamily: *Saccharomyces cerevisiae* hypothetical protein YDR348c

Query Match

Best Local Similarity 33.7%; Score 44.5; DB 2; Length 499;

Matches 10; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

QY 1

1 PLHNQEVTAEDGTQRA---EKCSKP 22

DB 164 PPSYEBITSTNGRRAYRKEVKVSRP 188

RESULT 23

E81715

ferredoxin [2Fe-2S] TC0329 [similarity] - *Chlamydia muridarum* (strain Nigg)C:Species: *Chlamydia muridarum*, *Chlamydia trachomatis* MoPn

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: E81715

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwin, M.; Nelson, W.; DeBoy, R.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A:Title: Genome sequences of *Chlamydia trachomatis* MoPn and *Chlamydia pneumoniae* AR39.

A:Reference number: A81500; MUID:20150255; PMID:10684935

A:Accession: E81715

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-91 <TET>

A:Cross-references: UNIPROT:Q9PKY1; UNIPARC:UPI00000578A9; GB:AE002300; GB:AE002160; NID

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0329

C:Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology

C:Keywords: 2Fe, 2S; metalloprotein

F:36,41,44,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match

Best Local Similarity 33.3%; Score 44; DB 2; Length 91;

Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4

4 NQEVTAEDGTQRAEKC 19

DB 12 NQEFLEDDGSPIAEAC 27

RESULT 24

AE3311

cytochrome c1 [imported] - *Brucella melitensis* (strain 16M)C:Species: *Brucella melitensis*

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AE3311

R;DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Los, T.; Ivanova,

.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitensis*

A:Reference number: AD3252; PMID:11756688

A:Accession: AE3311

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-268 <KUR>

A:Cross-references: UNIPROT:Q8YIG9; UNIPARC:UPI0000057CC6; GB:AE008917; PIDN:AAL51656.1

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BME10475

A:Map position: 1

C:Superfamily: cytochrome c1 heme protein; cytochrome c1 heme protein homology

C:Keywords: chromoprotein; heme; iron; metalloprotein

F:53.56/Binding site: heme (Cys) (covalent) #status predicted

F:57/Binding site: heme iron (His) (axial ligand) #status predicted

Query Match

Best Local Similarity 33.3%; Score 44; DB 2; Length 268;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1

1 PLHNQEVTAEDGT 13

DB 199 PLSDSQVTYEDGT 211

RESULT 25

PH1917

FL-160-1 protein - *Trypanosoma cruzi* (fragment)C:Species: *Trypanosoma cruzi*

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C:Accession: PH1917

R;Van Voorhis, W.C.; Barrett, L.; Koelling, R.; Farr, A.G.

J. Exp. Med. 178, 681-694, 1993

A:Title: FL-160 proteins of *Trypanosoma cruzi* are expressed from a multigene family and

A:Reference number: JH0823; MUID:93340646; PMID:7688032

A:Accession: PH1917

A:Molecule type: DNA

A:Residues: 1-288 <VAN>

A:Cross-references: UNIPROT:Q03832; UNIPARC:UPI000017B5AE

C:Keywords: glycoprotein

Query Match

Best Local Similarity 33.3%; Score 44; DB 2; Length 288;

Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 3

3 HNQEVTAEDGTQRAEKCSP 22

DB 269 HSTEVASVDGATGPGNCSR 288

RESULT 26

T09024

proline-rich protein T27E11.90 - *Arabidopsis thaliana*C:Species: *Arabidopsis thaliana* (mouse-ear cross)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09024

R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft,

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16533

A:Accession: T09024

A:Molecule type: DNA

A:Residues: 1-577 <BEV>

A:Cross-references: UNIPROT:Q9STP1; UNIPARC:UPI00000A3C75; EMBL:AL078579; GSPDB:GN00062,

A:Experimental source: cultivar Columbia; BAC clone T27E11

C:Genetics:

A:Gene: AtSP.T27E11.90

A:Map position: 4

A:Introns: 26/1; 117/1; 338/1; 411/3; 430/2; 498/2

Query Match

Best Local Similarity 33.3%; Score 44; DB 2; Length 577;

Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 H N Q E V T A E D G T Q R A E 17
| : | | | | : | |
Db 17 H S S N S T A S D G T E R E E 31

RESULT 27

T40625
single-stranded DNA-binding protein 68k chain [validated] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40625; T46571
R:Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z21941

Query Match 33.3%; Score 44; DB 2; Length 609;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches 8; Conservative 5; Mismatches 5; Indels

RESULT 28

replication protein A1 homolog T19B16.100 - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C.Accession: T04434
 R.Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansonge, W.; Bancroft, I.; Mewes, H.W.
 submitted to the Protein Sequence Database. April 1998

Query Match 33.3%; Score 44; DB 2; Length 717;
Best Local Similarity 72.7%; Pred. No. 1.5e+02;
Matches 8: Conservative 0; Mismatches 3; Indels

RESULT 29
C95367

C35367
conserved hypothetical protein Smal548 [imported] - *Sinorhizobium meliloti* (strain 1021)
C:Species: *Sinorhizobium meliloti*
C:date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 16-Aug-2004
C:Accession: C953367
R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hublet, F.; Bow
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:title: Nucleotide sequence and predicted functions of the entire *Sinorhizobium meliloti*
A:Reference number: A95262; PMID:21396509; PMID:11481432

Query Match 33.3%; Score 44; DB 2; Length 1051;
Best Local Similarity 42.1%; Pred. No. 2.1e+02;
Matches 8; Conservative 3; Mismatches 8; Indels

RESULT, T 30

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type gamma - chicken
 C-Species: Gallus gallus (chicken)
 C-Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C-Accession: T42636
 R-Qinghua, X.; Xiaojun, G.; Cong, S.; Zong, S.M.; Jong, Y.J.; Chan, J.; Wang, L.H.
 submitted to the EMBL Data Library, October 1995
 A-Reference number: Z42226

Query Match	33.3%	Score 44;	DB 2;	Length 1422;
Best Local Similarity	50.0%	Pred. No. 2.8e+02;		
Matches	9;	Conservative	2;	Mismatches 7;
				Indels

RESULT 31

RESOL 31
W1WL5
E1 protein - human papillomavirus type 5b
C:Species: human papillomavirus type 5b

```
A>Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: A40480
R:Yabe, Y.; Sakai, A.; Hisumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A:Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic segment amplifi
A:Reference number: A40480; MUID:91306467; PMID:1649510
C:Accession: A40480
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-606 <YAB>
A:Cross-references: UNIPROT:P26542; UNIPARC:UPI0000138316; GB:D90252; NID:G222395; PIDN:
C:Superfamily: papillomavirus E1 protein
C:Keywords: early protein

Query Match      33.0%; Score 43.5; DB 1; Length 606;
Best Local Similarity 55.0%; Pred. No. 1.5e+02;
Matches 11; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY      2 LHNQEVTAEDG-TQRAEKCS 20
      ||| ||| ||| ||| ||| |||
Db      579 LSDQEEEGDGSQRAFCQS 598

RESULT 32
I52603
MPS1 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
A:Accession: I52603
R:Spillsbury, K.; O'Mara, M.A.; Wu, W.M.; Rowe, P.B.; Symonds, G.; Takayama, Y.
Blood 85, 1620-1629, 1995
A:Title: Isolation of a novel macrophage-specific gene by differential cDNA analysis.
A:Reference number: I52603; MUID:95195232; PMID:7888681
A:Accession: I52603
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-661 <RES>
A:Cross-references: UNIPROT:Q61889; UNIPARC:UPI00002910D; GB:L20315; NID:G431419; PIDN:

Query Match      33.0%; Score 43.5; DB 2; Length 661;
Best Local Similarity 43.5%; Pred. No. 1.6e+02;
Matches 10; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

QY      1 PLHNQEVTAEDGTQRAEKCKPC 23
      ||| ||| ||| ||| ||| |||
Db      414 PVHLLSQTHEGYSLRE-CKKKC 435

RESULT 33
S60588
drebrin A - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S60588
R:Shirao, T.; Kojima, N.; Obata, K.
Neuroreport 3, 109-112, 1992
A:Title: Cloning of drebrin A and induction of neurite-like processes in drebrin-transfe
A:Reference number: S60588; MUID:92305233; PMID:1611026
A:Accession: S60588
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-707 <SHI>
A:Cross-references: UNIPROT:Q07266; UNIPARC:UPI0000129878; EMBL:X59267; NID:G297820; PID

Query Match      33.0%; Score 43.5; DB 2; Length 707;
Best Local Similarity 30.6%; Pred. No. 1.7e+02;
Matches 11; Conservative 5; Mismatches 7; Indels 13; Gaps 1;

QY      2 LHNQEVTAEDGTQRAE-----KCSKPCA 24
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      637 LTNGETTQEGTQQAASEGYFSQSQEETFAQSEPC 672
```

```
RESULT 34
G71562
ferredoxin [2Fe-2S] IV [similarity] - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: G71562
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: G71562
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <ARN>
A:Cross-references: UNIPROT:O84062; UNIPARC:UPI00000D70D8; GB:AE001280; GB:AE001273; NID:
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: fer
C:Superfamily: ferredoxin [2Fe-2S]; ferredoxin [2Fe-2S] homology
C:Keywords: 2Fe-2S; metalloprotein
F:23-79/Domain: ferredoxin [2Fe-2S] homology <FER>
F:36,41,44,78/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match      32.6%; Score 43; DB 2; Length 91;
Best Local Similarity 56.2%; Pred. No. 28;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      4 NOEVTAEADGTQRAEKC 19
      ||| ||| ||| |||
Db      12 NOEPHLEDGSSIAEVC 27

RESULT 35
I39734
CBS domain-containing protein - Anabaena variabilis
N:Alternate names: hypothetical protein 3
C:Species: Anabaena variabilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S68184; I39734
R:Schmitz, O.; Boison, G.; Hilscher, R.; Hundeshagen, B.; Zimmer, W.; Lottspeich, F.; B
Eur. J. Biochem. 233, 266-276, 1995
A:Title: Molecular biological analysis of a bidirectional hydrogenase from cyanobacteri
A:Reference number: I39730; MUID:96061958; PMID:7588754
A:Accession: S68184
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-199 <SCH>
A:Cross-references: UNIPROT:Q44516; UNIPARC:UPI00000B4811; EMBL:X79285; NID:G1032475; P
A:Experimental source: ATCC 29413
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
C:Superfamily: uncharacterized protein with CBS and CP12 domains; CBS homology
C:Keywords: duplication
F:11-60/Domain: CBS homology <CBS1>
F:78-124/Domain: CBS homology <CBS2>

Query Match      32.6%; Score 43; DB 1; Length 199;
Best Local Similarity 58.8%; Pred. No. 60;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      5 QEVTAEDGTQRAEKCSK 21
      ||| ||| ||| ||| |||
Db      167 EEMQAEAMAHQRAEKVSK 183

RESULT 36
AC1902
hypothetical protein alr0765 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AC1902
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
```


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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:35:08 ; Search time 159.273 Seconds
(without alignment)
106.312 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLNNQEVTAEDGTQRAEKCKPKCA 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	97.0	419	2	Q9UK79 homo sapien
2	128	97.0	1255	1	ERBB2_HUMAN
3	121	91.7	1259	1	ERBB2_CANFA
4	114	86.4	711	2	Q80B89_MOUSE
5	114	86.4	1257	1	ERBB2_RAT
6	114	86.4	1259	2	Q8K3F9_RAT
7	114	86.4	1305	2	Q6ZPE0_MOUSE
8	113	85.6	1254	1	ERBB2_MESAU
9	55	41.7	1195	2	Q4RV10_TETNG
10	54	40.9	92	1	SGPI_SCHGR
11	52	39.4	273	1	OLRI_HUMAN
12	51	38.6	498	2	Q7S109_NEUCR
13	50.5	38.3	670	2	Q4QG99_LEIMA
14	50	37.9	676	2	Q59F42_HUMAN
15	50	37.9	686	1	2NF7_HUMAN
16	50	37.9	686	2	Q5R8X0_PONPY
17	50	37.9	944	2	Q6CNE1_KLUILA
18	49	37.1	74	2	Q9N0X1_RABIT
19	49	37.1	116	2	Q9BG67_RABIT
20	49	37.1	147	1	VXIS_BPSF5
21	49	37.1	405	2	Q6RGS5_HUMAN
22	49	37.1	645	2	Q6RGS6_HUMAN
23	49	37.1	1081	2	Q59FL8_HUMAN
24	49	37.1	1091	2	Q504U8_HUMAN
25	49	37.1	1209	2	Q8MIL8_PIG
26	49	37.1	1210	1	EGFR_HUMAN
27	49	37.1	1913	2	Q52PE0_MAGGR
28	48.5	36.7	324	2	Q90XJ6_LATWE
29	48.5	36.7	514	2	Q6JQ08_LATWE
30	48.5	36.7	912	2	Q6TIH0_LATWE
31	48	36.4	103	2	Q5M840_RAT

32	48	36.4	150	2	Q6IGT7_DROME
33	48	36.4	214	2	Q8XDI3_ECO57
34	48	36.4	269	2	Q83LE8_SHIFL
35	48	36.4	270	2	Q87503_ECOLI
36	48	36.4	468	2	Q4QBD3_LEIMA
37	48	36.4	478	2	Q9ESE0_RAT
38	48	36.4	632	2	Q6NKT4_ARATH
39	48	36.4	643	2	Q9ERV6_MOUSE
40	48	36.4	644	2	Q23J21_ARATH
41	48	36.4	655	2	Q9WVF5_MOUSE
42	48	36.4	882	2	Q6XOM1_9STRA
43	48	36.4	1209	2	Q9QX70_RAT
44	48	36.4	1210	1	EGFR_MOUSE
45	48	36.4	1210	2	Q9EP98_MOUSE
46	48	36.4	1210	2	Q5SVE8_MOUSE
47	48	36.4	1244	2	Q93330_CAEEL
48	48	36.4	1435	1	TRS85_HUMAN
49	48	36.4	1445	2	Q4QG46_LEIMA
50	47.5	36.0	449	2	Q5XGJ3_XENTR
51	47.5	36.0	482	2	Q7RE84_PLAYO
52	47	35.6	64	2	Q615E1_CAEBR
53	47	35.6	280	2	Q5BIC0_EMENT
54	47	35.6	500	2	Q4K516_PSEF5
55	47	35.6	572	2	Q9AU64_ELAGV
56	47	35.6	573	2	Q8BZU6_MOUSE
57	47	35.6	655	1	TNR21_MOUSE
58	47	35.6	655	2	Q543Y9_MOUSE
59	47	35.6	684	2	Q7Q2B5_ANOGA
60	47	35.6	722	2	Q9DC42_MOUSE
61	47	35.6	772	2	Q6MYK9_ASFPU
62	47	35.6	774	2	Q80379_DAUCA
63	47	35.6	777	2	Q7QVA9_GIALA
64	47	35.6	811	2	Q4QB17_LEIMA
65	47	35.6	987	2	Q8MR93_DROME
66	47	35.6	987	2	Q9V7X1_DROME
67	46.5	35.2	77	2	Q4AR26_AVIMR
68	46.5	35.2	284	2	Q4H3J8_CIOIN
69	46.5	35.2	450	2	Q7X2U6_9BACT
70	46	34.8	66	2	Q6V7P8_9CAUD
71	46	34.8	184	2	Q98NF4_RHILU
72	46	34.8	195	2	Q96VJ6_KLUZA
73	46	34.8	224	2	Q4IA61_GIBZE
74	46	34.8	314	2	Q5AK03_CANAL
75	46	34.8	580	2	Q6F756_ACIALD
76	46	34.8	651	2	Q98SM6_CHICK
77	46	34.8	662	2	Q5X128_BRARE
78	46	34.8	678	2	Q5REJ3_PONPY
79	46	34.8	937	2	Q623H8_ORYSA
80	46	34.8	963	2	Q7XL40_ORYSA
81	46	34.8	974	2	Q8LNB2_ORYSA
82	46	34.8	1195	2	Q7XQZ1_ORYSA
83	46	34.8	1390	1	INSR_AEDAE
84	46	34.8	1449	2	Q8S5K3_ORYSA
85	46	34.8	1461	2	Q7XGE3_ORYSA
86	46	34.8	1466	2	Q7XGE5_ORYSA
87	46	34.8	1661	2	Q7XGE6_ORYSA
88	46	34.8	2647	2	Q90580_PLAFA
89	45.5	34.5	436	2	Q4Z8N7_PIG
90	45.5	34.5	474	2	Q8G4D3_BIFLO
91	45.5	34.5	704	2	Q9DA98_MOUSE
92	45.5	34.5	709	2	Q9AP25_MOUSE
93	45	34.1	174	2	Q8SA72_ORYSA
94	45	34.1	179	2	Q6B8H4_9ACAR
95	45	34.1	196	2	Q7RUC9_NEUCR
96	45	34.1	205	2	Q26554_SCHMA
97	45	34.1	231	2	Q8K5B9_MOUSE
98	45	34.1	264	2	Q7XBH7_ORYSA
99	45	34.1	289	2	Q6FRM9_CANGA
100	45	34.1	303	2	Q8TWD2_METKA

ALIGNMENTS

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RESULT 1
Q9UK79 HUMAN
ID Q9UK79_HUMAN PRELIMINARY; PRT; 419 AA.
AC Q9UK79
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herstatin.
GN Name=HER-2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99415951; PubMed=10485918; DOI=10.1073/pnas.96.19.10869;
RA Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
RT "The HER-2/neu receptor tyrosine kinase gene encodes a secreted
RT autoinhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Henner W.D.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177761; AAD56009.2; -; mRNA.
DR HSSP; P04626; 1N8Z.
DR SNR; Q9UK79; 23-345.
DR Ensemble; ENSG00000141736; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IDA.
DR GO; GO:0004715; F:non-membrane spanning protein tyrosine kina. ; IDA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. ; IDA.
DR InterPro; IPR000494; EGRF_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin_repeat.
DR Pfam; PF00757; Furin-like; 1.
DR SMART; SM00261; FU; 1.
SQ SEQUENCE 419 AA; 45472 MW; FEC1BE347E2D030C CRC64;

Query Match 97.0%; Score 128; DB 2; Length 419;
Best Local Similarity 95.8%; Pred. No. 4,le-11;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 PLHNQVETADGTQRAEKCSPCA 24
   |||||
Db 316 PLHNQVETADGTQRAEKCSPCA 339

RESULT 2
ERBB2 HUMAN
ID ERBB2 HUMAN STANDARD; PRT; 1255 AA.
AC P04626; Q14256; Q6LDV1; Q9UMK4;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Receptor tyrosine-protein kinase erbB-2 precursor (BC 2.7.1.112)
DE (p18erBB2) (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell
DE surface receptor HER2) (MLN 19).
GN Name=ERBB2; Synonyms=HER2, NEU, NGL;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=86118663; PubMed=3003577;
RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
RA Saito T., Toyoshima K.;
RT "Similarity of protein encoded by the human c-erb-B-2 gene to
RT epidermal growth factor receptor.";
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RL Nature 319:230-234 (1986).
RN [2]
RP NUCLEOTIDE SEQUENCE, AND VARIANT ALA-1170.
RX MEDLINE=86070181; PubMed=2999974;
RA Cousens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J.,
RA Seeburg P.H., Libermann T.A., Schlessinger J., Francke U.,
RA Levinson A., Ullrich A.;
RT "Tyrosine kinase receptor with extensive homology to EGF receptor
RT shares chromosomal location with neu oncogene.";
RL Science 230:1132-1139 (1985).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND
RP ALA-1170.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE OF 1-191.
RX MEDLINE=87286898; PubMed=3039351;
RA Tal M., King C.R., Kraus M.H., Ullrich A., Schlessinger J., Givol D.;
RT "Human HER2 (neu) promoter: evidence for multiple mechanisms for
RT transcriptional initiation.";
RL Mol. Cell. Biol. 7:2597-2601 (1987).
RN [5]
RP NUCLEOTIDE SEQUENCE OF 737-1031.
RX MEDLINE=86016729; PubMed=2995967;
RA Semba K., Kamata N., Toyoshima K., Yamamoto T.;
RT "A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-
RT erbB-1/epidermal growth factor-receptor gene and is amplified in a
RT human salivary gland adenocarcinoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501 (1985).
RN [6]
RP NUCLEOTIDE SEQUENCE OF 832-909.
RX TISSUE=Mammary carcinoma;
RX MEDLINE=85272597; PubMed=2992089;
RA King C.R., Kraus M.H., Aaronson S.A.;
RT "Amplification of a novel v-erbB-related gene in a human mammary
RT carcinoma.";
RL Science 229:974-976 (1985).
RN [7]
RP NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.
RX MEDLINE=94000386; PubMed=8104414;
RA Sarkar F.H., Ball D.E., Li Y.W., Criseman J.D.;
RT "Molecular cloning and sequencing of an intron of Her-2/neu (ERBB2)
RT gene.";
RL DNA Cell Biol. 12:611-615 (1993).
RN [8]
RP IDENTIFICATION IN A COMPLEX WITH PIK3C2A AND EGFR, IDENTIFICATION IN A
RP COMPLEX WITH PIK3C2B AND EGFR, AND INTERACTION WITH PIK3C2B.
RX PubMed=10805725;
RA Arcaro A., Zvelebil M.J., Wallasch C., Ullrich A., Waterfield M.D.,
RA Domin J.;
RT "Class II phosphoinositide 3-kinases are downstream targets of
RT activated polypeptide growth factor receptors.";
RL Mol. Cell. Biol. 20:3817-3830 (2000).
RN [9]
RP INTERACTION WITH PLXNB1.
RX PubMed=15210733; DOI=10.1093/jcb.200312094;
RA Swiercz J.M., Kumer R., Offermanns S.;
RT "Plexin-B1/RhoGEF-mediated RhoA activation involves the receptor
RT tyrosine kinase ErbB-2.";
RL J. Cell Biol. 165:869-880 (2004).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 654-662 IN COMPLEX WITH HLA
RP AND BETA-2 MICROGLOBULIN.
RX MEDLINE=20062861; PubMed=10593938; DOI=10.1074/jbc.274.51.36422;
RA Kuhns J.J., Batalia M.A., Yan S., Collins E.J.;
RT "Poor binding of a HER-2/neu epitope (GP2) to HLA-A2.1 is due to a
RT lack of interactions with the center of the peptide.";
RL J. Biol. Chem. 274:36422-36427 (1999).
```

DR GO:00030879; P:mammary gland development; TAS.
DR GO:0007399; P:neurogenesis; TAS.
DR GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO:00045765; P:regulation of angiogenesis; NAS.
DR GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; NAS.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR 3D-structure; ATP-binding; Glycoprotein; Kinase; Multigene family;
KW Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 1255 Receptor tyrosine-protein kinase erbb-2.
FT TOPO_DOM 22 652 Extracellular (Potential).
FT TRANSMEM 653 675 Potential.
FT TOPO_DOM 676 1255 Cytoplasmic (Potential).
FT DOMAIN 720 987 protein kinase.
FT NP_BIND 726 734 ATP (By similarity).
Query Match 97.0%; Score 128; DB 1; Length 1255;
Best Local Similarity 95.8%; Pred. NO. 1.3e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNQEVTAEDGTQRAEKCKSPCA 24
DB 316 PLHNQEVTAEDGTQRAEKCKSPCA 339
RESULT 3
ERBB2_CANFA
ID ERBB2_CANFA STANDARD; PRT; 1259 AA.
AC O18735;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Receptor tyrosine-protein kinase erbb-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (C-erbB-2).
GN Name=ERBB2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Mammary gland;
RA Yokota H.;
RT "CDNA cloning of erbb-2 from canine mammary gland.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Essential component of a neuroligin-receptor complex,
CC although neuroligins do not interact with it alone. Gp30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (Potential). Interacts with PRKCAPB. Binds PLXNB1.
CC Part of a complex with EGFR and either PIK3C2A or PIK3C2B. May
CC interact with PIK3C2B when phosphorylated on Tyr-1196.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC (By similarity).
CC -!- POLYMORPHISM: There are four alleles due to the variations in
CC positions 654 and 655. Allele B1 (Ile-654/Ile-655) has a frequency
CC of 0.782; allele B2 (Ile-654/Val-655) has a frequency of 0.206;
CC allele B3 (Val-654/Val-655) has a frequency of 0.012.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; M11767; AAA35808.1; -; Genomic DNA.
DR EMBL; M11761; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11762; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11763; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11764; AAA35808.1; JOINED; Genomic DNA.
DR EMBL; M11765; AAA35808.1; JOINED; Genomic DNA.
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DR EMBL; M11730; AAA75493.1; -; mRNA.
DR EMBL; M12036; AAA35978.1; -; Genomic DNA.
DR EMBL; AY208911; AA018082.1; -; Genomic DNA.
DR EMBL; X03363; CA27060.1; -; mRNA.
DR EMBL; M16792; AAAS8637.1; -; Genomic DNA.
DR EMBL; M16799; AAAS8637.1; JOINED; Genomic DNA.
DR EMBL; M16790; AAAS8637.1; JOINED; Genomic DNA.
DR EMBL; M16791; AAAS8637.1; JOINED; Genomic DNA.
DR EMBL; L23195; AAA35809.1; -; Genomic DNA.
DR EMBL; M95667; AAC37531.1; -; Unassigned DNA.
DR PIR; A24571; A24571.
DR PDB; 1NBZ; X-ray; C=23-629.
DR PDB; 1OVC; Model; A=737-1031.
DR PDB; 1S78; X-ray; A/B=23-646.
DR Ensembl; ENSG00000141736; Homo sapiens.
DR HGNC; HGNC:3430; ERBB2.
DR MIM; 164870; -;
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; NAS.
DR GO; GO:0043125; F:Erbb-3 class receptor binding; TAS.
DR GO; GO:0046382; F:protein heterodimerization activity; NAS.
DR GO; GO:0004716; F:receptor signaling protein tyrosine kinase . . ; TAS.
DR GO; GO:0008283; P:cell proliferation; TAS.
DR GO; GO:0007507; P:heart development; TAS.

DR GO:00030879; P:mammary gland development; TAS.
DR GO:0007399; P:neurogenesis; TAS.
DR GO:0048015; P:phosphoinositide-mediated signaling; NAS.
DR GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO:00045765; P:regulation of angiogenesis; NAS.
DR GO:0007169; P:transmembrane receptor protein tyrosine kin. . ; NAS.
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DR InterPro; IPR006212; Furin repeat.
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DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR 3D-structure; ATP-binding; Glycoprotein; Kinase; Multigene family;
KW Nucleotide-binding; Phosphorylation; Polymorphism; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
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FT TOPO_DOM 676 1255 Cytoplasmic (Potential).
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Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3
ERBB2_CANFA
ID ERBB2_CANFA STANDARD; PRT; 1259 AA.
AC O18735;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
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DE Receptor tyrosine-protein kinase erbb-2 precursor (EC 2.7.1.112)
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GN Name=ERBB2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
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CC although neuroligins do not interact with it alone. Gp30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin (By similarity).
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CC tyrosine phosphate.
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (Potential). Interacts with PRKCAPB. Binds PLXNB1. Part of a
CC complex with EGFR and either PIK3C2A or PIK3C2B. May interact with
CC PIK3C2B when phosphorylated on Tyr-1196.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.

CC PIK3C2B when phosphorylated on Tyr-1200 (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC (By similarity).
CC -|- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AB008451; BAA23127.1; -; mRNA.
CC DR HSSP; P04626; 1N82.
CC DR SMR; O18735; 23-628.
CC DR Ensembl; ENSCARG00000016351; Canis familiaris.
CC DR InterPro; IPR000494; EGFR_L.
CC DR InterPro; IPR006211; Furin-like.
CC DR InterPro; IPR006212; Furin repeat.
CC DR InterPro; IPR000719; Prot Kinase.
CC DR InterPro; IPR001245; Tyr_Pkinase.
CC DR InterPro; IPR008266; Tyr_Pkinase_AS.
CC DR InterPro; IPR004019; YLP_motif.
CC DR Pfam; PF00757; Furin-like; 1.
CC DR Pfam; PF02757; Recep_L_domain; 2.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Prot_kinase; 1.
CC DR SMART; SM00261; FU; 3.
CC DR SMART; SM00219; TyrKc; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC KW ATP-binding; Glycoprotein; Kinase; Multigene family;
KW Nucleotide-binding; Phosphorylation; Receptor; Signal; Transferase;
KW Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 22 Potential.
FT CHAIN 23 1259 Receptor tyrosine-protein kinase erbB-2.
FT TOPO_DOM 23 653 Extracellular (Potential).
FT TRANSMEM 654 674 Potential.
FT TOPO_DOM 675 1259 Cytoplasmic (Potential).
FT DOMAIN 719 986 Protein kinase.
FT NP_BIND 725 1231 ATP (By similarity).
FT REGION 1199 1201 Interaction with PIK3C2B (By similarity).
FT COMPIAS 192 268 Cys-rich.
FT COMPART 1101 1219 Pro-rich.
FT ACT_SITE 844 844 By similarity.
FT BINDING 752 752 ATP (By similarity).
FT MOD_RES 1138 1138 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT MOD_RES 1200 1200 Phosphotyrosine (Potential).
FT MOD_RES 1252 1252 Phosphotyrosine (by autocatalysis) (By
FT similarity).
FT CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 259 259 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 421 421 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 529 529 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 570 570 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 628 628 N-linked (GlcNAc...) (Potential).
FT DISULFID 195 204 By similarity.
FT DISULFID 199 212 By similarity.
FT DISULFID 220 227 By similarity.
FT DISULFID 224 235 By similarity.
FT DISULFID 236 244 By similarity.
FT DISULFID 240 252 By similarity.
FT DISULFID 255 264 By similarity.
FT DISULFID 268 295 By similarity.
FT DISULFID 299 311 By similarity.
FT DISULFID 315 331 By similarity.
FT DISULFID 334 338 By similarity.
FT DISULFID 511 519 By similarity.
FT DISULFID 514 527 By similarity.

FT DISULFID 530 539 By similarity.
FT DISULFID 543 559 By similarity.
FT DISULFID 562 575 By similarity.
FT DISULFID 566 583 By similarity.
FT DISULFID 586 595 By similarity.
FT DISULFID 599 622 By similarity.
FT DISULFID 625 633 By similarity.
FT DISULFID 629 641 By similarity.
SQ SEQUENCE 1259 AA; 137991 MW; E37364D49C4ACD46 CRC64;
Query Match 91.7%; Score 121; DB 1; Length 1259;
Best Local Similarity 91.7%; Pred. No. 1.6e-09;
Matches 22; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 PLHNOEVTAE DGTORAEKCSKPCA 24
Db 316 PLHNOEVTAE DGTQRCCKSKPCA 339

RESULT 4
Q80Y89 MOUSE
ID Q80Y89_MOUSE PRELIMINARY; PRT; 711 AA.
AC Q80Y89;
CT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE V-erb-b2 erythroblastic leukemia viral oncogene homolog 2,
DE neuro/glioblastoma derived oncogene homolog, isoform 2.
GN Name=ErbB2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Sosne M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield A.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC046811; AAH46811.1; -; mRNA.
DR EMBL; BC053078; AAH53078.1; -; mRNA.
DR HSSP; P06494; 1N8Y.
DR SMR; Q80Y89; 23-630.
DR Ensembl; ENSMUSG000000062312; Mus musculus.

```

DR MGI; MGI:95410; Erbb2.
DR GO; GO:0016324; C:apical plasma membrane; IDA.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007507; P:heart development; IMP.
DR GO; GO:0042552; P:myelination; IMP.
DR GO; GO:0007422; P:peripheral nervous system development; IMP.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin-repeat.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR SMART; SM00261; FU; 4.
SQ SEQUENCE 711 AA; 78707 MW; 682B188EB0E71318 CRC64;

Query Match      86.48; Score 114; DB 2; Length 711;
Best Local Similarity 87.58; Pred.No. 1.1e-08;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PLNQEVTAEDGTQRAEKCKPKCA 24
   | : ||||| ||||| ||||| |||||
Db 317 PPNQEVTAEDGTQRAEKCKPKCA 340

RESULT 5
ERBB2 RAT
ID ERBB2 RAT STANDARD; PRT; 1257 AA.
AC P06494; Q6P732;
DC 01-DEC-1998 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Epidermal growth factor
DE receptor-related protein).
DE Name=Erbb2; Synonyms=Neu;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Neuroblastoma;
RX MEDLINE=96118662; PubMed=3945311;
RA Bargmann C.I., Hung M.-C., Weinberg R.A.;
RT "The neu oncogene encodes an epidermal growth factor receptor-related
RT protein.";
RL Nature 319:226-230(1986).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Prostate;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE OF 634-699.
RX MEDLINE=92035293; PubMed=1682063;
RA Masui T., Mann A.M., Macatee T.L., Garland E.M., Okamura T.,
RA Smith R.A., Cohen S.M.;
RT "Direct DNA sequencing of the rat neu oncogene transmembrane domain
RT reveals no mutation in urinary bladder carcinomas induced by N-butyl-
RT N-(4-hydroxybutyl)nitrosamine, N-[4-(5-nitro-2-furyl)-2-
RT thiazolyl]formamide or N-methyl-N-nitrosourea.";
RL Carcinogenesis 12:1975-1978(1991).
RN [4]
RP NUCLEOTIDE SEQUENCE OF 852-905.
RC TISSUE=Sciatic nerve;
RX MEDLINE=91222560; PubMed=2025425; DOI=10.1016/0896-6273(91)90167-X;
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially
RT expressed in the vertebrate nervous system.";
RL Neuron 6:691-704(1991).
RN [5]
RP STRUCTURE BY NMR OF 650-668.
RX MEDLINE=92155181; PubMed=1346763;
RA Gullick W.J., Bottomley A.C., Loftis F.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.E., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-
RT oncogenic and oncogenic forms of the neu protein.";
RL EMBO J. 11:43-48(1992).
CC -1- FUNCTION: Essential component of a neurotulin-receptor complex,
CC allthough neurotulin do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC constitutively activated oncogenic variant forms a homodimer.
CC Interacts with PRKCAP and PLXNB1. Part of a complex with EGFR and
CC either PIK3C2A or PIK3C2B. May interact with PIK3C2B when
CC phosphorylated on Tyr-1198 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine residues
CC (By similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X03362; CAA27059.1; ALT_INIT; mRNA.
CC EMBL; BC061863; AAH61863.1; ALT_INIT; mRNA.
CC PIR; A24562; TVRTNU.
CC PDB; 1N8Y; X-ray; C=23-631.
CC Ensembl; ENSRNOG00000006450; Rattus norvegicus.
CC RCD; 2561; Erbb2.
CC GO; GO:0045595; P:regulation of cell differentiation; TAS.
CC GO; GO:0042127; P:regulation of cell proliferation; TAS.
CC InterPro; IPR000494; EGFR_L.
CC InterPro; IPR006211; Furin-like.
CC InterPro; IPR006212; Furin-repeat.
CC InterPro; IPR00719; Prot_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_pkinase_AS.
CC InterPro; IPR004019; YLP_motif.
CC Pfam; PF00757; Furin-like; 1.
CC Pfam; PF01030; Recep_L_domain; 2.
CC Pfam; PF02757; YLP; 2.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00261; FU; 4.
CC SMART; SM00219; TyrcK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS50109; PROTEIN_KINASE_TYR; 1.
CC 3D-structure; ATP-binding; Disease mutation; Glycoprotein; Kinase;
KW Multigene family; Nucleotide-binding; Phosphorylation; Proto-oncogene;
KW Receptor; Signal; Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 1257 Receptor tyrosine-protein kinase erbB-2.
FT TOPO_DOM 22 654 Extracellular (Potential).
FT TRANSMEM 655 677 Potential.
FT TOPO_DOM 678 1257 Cytoplasmic (Potential).
FT DOMAIN 722 989 Protein kinase.
FT NP_BIND 728 1197 ATP (By similarity).
FT REGION 1197 1199 Interaction with PIK3C2B (By similarity).
FT COMEBIAS 159 369 Cys-rich.
FT COMEBIAS 473 646 By similarity.
FT ACT_SITE 847 847 ATP (By similarity).
FT BINDING 755 755 Phosphotyrosine (by autocatalysis) (By
FT MOD_RES 1141 1141 similarity).
FT MOD_RES 1198 1198 Phosphotyrosine (Potential).
FT MOD_RES 1250 1250 Phosphotyrosine (by autocatalysis) (By

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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 4.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Kinase; Nucleotide-binding; Transferase.
FT NON TER 1
SQ SEQUENCE 1305 AA; 143508 MW; A51D897408521860 CRC64;

Query Match      86.4%; Score 114; DB 2; Length 1305;
Best Local Similarity 87.5%; Pred. No. 2.le-08;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 PLHNOEVTAEADGTORAEKCSKPCA 24
Db 366 PPNQOEVTAEADGTORCEKCSKPCA 389

RESULT 8
ERBB2 MESAU STANDARD; PRT; 1254 AA.
AC Q60553;
DT 15-DEC-1998 (Rel. 37, Created)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene).
GN Name=ERBB2; Synonym=NEU;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Cricetidae; Cricetinae; Mesocricetus.
OX NCBI_TaxID=10036;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Nerve;
RC MEDLINE=94193007; PubMed=7908275; DOI=10.1016/0378-1119(94)90553-3;
RA Nakamura T.; Ushijima T.; Ishizaka Y.; Nagao M.; Arai M.; Yamazaki Y.;
RA Ishikawa T.;
RT "Cloning and activation of the Syrian hamster neu proto-oncogene.";
RL Gene 140:251-255(1994).
CC -!- FUNCTION: Essential component of a neurotrophin-receptor complex,
CC although neurotrophins do not interact with it alone. Gp30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC tyrosine phosphate.
CC -!- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (Potential). Part of a complex with EGFR and either PIK3C2A or
CC PIK3C2B. Interacts with PRKCA and PLXNB1. May interact with
CC PIK3C2B when phosphorylated on Tyr-1196 (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues.
CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. EGF receptor
CC subfamily.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; D16295; BAA03801.1; -; mRNA.
CC PIR; I48161; I48161.
CC HSPSP; P06494; IN8Y.
CC SMR; Q60553; 23-629.
CC InterPro; IPR000494; EGFR_L.
CC InterPro; IPR006211; Furin-like.
CC InterPro; IPR006212; Furin repeat.
CC InterPro; IPR000719; Prot_Kinase.
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```
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR InterPro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PF02757; YLP; 2.
DR ProDom; PD000001; TYRKINASE.
DR SMART; SM00261; FU; 4.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Disease mutation; Glycoprotein; Kinase; Multigene family;
KW Nucleotide-binding; Phosphorylation; Proto-oncogene; Receptor; Signal;
KW Transferase; Transmembrane; Tyrosine-protein kinase.
FT SIGNAL 1 21
FT CHAIN 22 1254
FT TOPO_DOM 22 652
FT TRANSMEM 653 675
FT TOPO_DOM 676 1254
FT DOMAIN 720 987
FT NP_BIND 726 734
FT REGION 1195 1197
FT COMPBIAS 158 368
FT COMPBIAS 472 644
FT ACT_SITE 845 845
FT BINDING 753 753
FT MOD_RES 1139 1139
FT MOD_RES 1196 1196
FT MOD_RES 1247 1247
FT CARBOHYD 68 68
FT CARBOHYD 125 125
FT CARBOHYD 187 187
FT CARBOHYD 259 259
FT CARBOHYD 530 530
FT CARBOHYD 571 571
FT CARBOHYD 629 629
FT DISULFID 195 202
FT DISULFID 199 212
FT DISULFID 236 244
FT DISULFID 240 252
FT DISULFID 255 264
FT DISULFID 268 295
FT DISULFID 299 311
FT DISULFID 315 331
FT DISULFID 334 338
FT DISULFID 511 520
FT DISULFID 515 528
FT DISULFID 531 540
FT DISULFID 544 560
FT DISULFID 563 576
FT DISULFID 567 584
FT DISULFID 587 596
FT DISULFID 600 623
FT DISULFID 626 634
FT DISULFID 630 642
FT VARIANT 658 658 V -> E (in oncogenic NEU).
FT VARIANT 659 659 V -> E (in oncogenic NEU).
SQ SEQUENCE 1254 AA; 138253 MW; 974C3791C21P2BE1 CRC64;

Query Match      85.6%; Score 113; DB 1; Length 1254;
Best Local Similarity 87.5%; Pred. No. 2.8e-08;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 PLHNOEVTAEADGTORAEKCSKPCA 24
Db 316 PLNNOEVTAEADGTORCEKCSKPCA 339

RESULT 9
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Q4RV10 TETNG
ID Q4RV10 TETNG PRELIMINARY; PRT; 1195 AA.
AC Q4RV10;
DT 13-SEP-2005 (TEMBLrel. 31, Created)
DT 13-SEP-2005 (TEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TEMBLrel. 31, Last annotation update)
DE Chromosome 12 SCAF14993, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00028560001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Fritsch J., Gardier G., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAEE01014993; CAG07772.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 1195 AA; 13325 MW; 52A41A36B3F6605E CRC64;

Query Match 41.7%; Score 55; DB 2; Length 1195;
Best Local Similarity 46.4%; Pred. No. 28;
Matches 13; Conservative 8; Mismatches 4; Indels 4; Gaps 1;

QY 1 PLHNQEVTAEDGTQRAEK-----CSKPCA 24
DB 961 PVNNNNVIQBDTYEWALKSWSPCKPCA 988

RESULT 10
SGPI_SCHGR
ID SGPI_SCHGR STANDARD; PRT; 92 AA.
AC Q46162;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Serine protease inhibitor I/II precursor [Contains: Protease inhibitor
DE SGPI-1 (Schistocerca gregaria trypsin inhibitor) (SGPI); Protease
DE inhibitor SGPI-2 (Schistocerca gregaria chymotrypsin inhibitor)
DE (SGCI)].
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE Ovary;
RX MEDLINE=98314507; PubMed=9652399;
RA Vanden Broeck J., Chiou S.-J., Schoofs L., Hamdaoui A.,

Vandenbussche F., Simonet G., Wataleb S., De Loof A.;
"Cloning of two cDNAs encoding three small serine protease inhibiting
peptides from the desert locust Schistocerca gregaria and analysis of
tissue-dependent and stage-dependent expression.";
Eur. J. Biochem. 254:90-95(1998).
RL [2]
RP PROTEIN SEQUENCE OF 20-54 AND 57-91, FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Ovary;
RX MEDLINE=98133320; PubMed=94751173; DOI=10.1016/S0014-5793(97)01585-8;
RA Hamdaoui A., Wataleb S., Devreese B., Chiou S.-J., Vanden Broeck J.,
RA Van Beumen J., De Loof A., Schoofs L.;
" Purification and characterization of a group of five novel peptide
serine protease inhibitors from ovaries of the desert locust,
RT Schistocerca gregaria.";
RL FEBS Lett. 422:74-78(1998).
RN [3]
RP STRUCTURE BY NMR OF 20-54 AND 57-91.
RX PubMed=11997226; DOI=10.1016/S1096-4959(01)00530-9;
RA Simonet G., Claeys I., Vanden Broeck J.;
"Structural and functional properties of a novel serine protease
RT inhibiting peptide family in arthropods.";
Comp. Biochem. Physiol. 132B:247-255(2002).
CC -! FUNCTION: In vitro, SGPI-1/SGCI is active against alpha-
CC chymotrypsin and trypsin while SGPI-2/SGRI is active against
CC alpha-chymotrypsin and pancreatic elastase.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! TISSUE SPECIFICITY: Expressed in hemolymph, ovaries, testes and
CC fat body of adults but are absent in the gut. Also present in
CC larval hemolymph and fat body.
CC -! SIMILARITY: Belongs to the protease inhibitor I19 family.
CC -! SIMILARITY: Contains 2 pacifastin repeats.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; Y09605; CAA70818.1; -; mRNA.
DR PDB; 1KGM; NMR; A=57-91.
DR PDB; 1KIO; NMR; A=57-91.
DR InterPro; IPR008037; Prot_inh_PMP.
DR Pfam; PF05375; Pacifastin_1; 2.
KW 3D-structure; Cleavage on pair of basic residues;
KW Direct protein sequencing; Protease inhibitor; Repeat;
KW Serine protease inhibitor; Signal.
FT SIGNAL 1 19
FT PEPTIDE 20 54 Protease inhibitor SGPI-1.
FT PEPTIDE 57 91 Protease inhibitor SGPI-2.
FT REPEAT 22 61 Pacifastin 1.
FT REPEAT 62 92 Pacifastin 2.
FT SITE 48 49 Reactive bond.
FT SITE 86 87 Reactive bond.
FT DISULFID 23 38
FT DISULFID 33 51
FT DISULFID 36 46
FT DISULFID 60 75
FT DISULFID 70 89
FT DISULFID 73 84
SQ SEQUENCE 92 AA; 9842 MW; 9E5A228C767C657C CRC64;

Query Match 40.9%; Score 54; DB 1; Length 92;
Best Local Similarity 50.0%; Pred. No. 2.6;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKCS 20
DB 52 PPHKEVTCPEGTTFDKCN 71

RESULT 11
OLR1_HUMAN
ID OLR1_HUMAN STANDARD; PRT; 273 AA.

```


AC P78380; Q72484;
 DT 13-SEP-2005 (rel. 48, Last sequence update)
 DT 13-SEP-2005 (rel. 48, Last annotation update)
 DE Oxidized low-density lipoprotein receptor 1 (Ox-LDL receptor 1)
 DE (Lectin-type oxidized LDL receptor 1) (Lectin-like oxidized LDL
 DE receptor 1) (Lectin-like oxLDL receptor 1) (LOX-1) [Contains:
 DE Oxidized low-density lipoprotein receptor 1, soluble form].
 GN Name=OLR1; Synonyms=LOX1;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], FUNCTION, AND TISSUE SPECIFICITY.
 RC TISSUE=Lung;
 RX MEDLINE=97205278; PubMed=9052782;
 RA Sawamura T., Kume N., Aoyama T., Moriaki H., Hoshikawa H., Aiba Y.,
 RA Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;
 RT "An endothelial receptor for oxidized low-density lipoprotein.";
 RL Nature 386:73-77(1997).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RX MEDLINE=98438416; PubMed=9763655;
 RA Li X., Bouzyk M.M., Wang X.;
 RT "Assignment of the human oxidized low-density lipoprotein receptor
 RT gene (OLR1) to chromosome 12p13.1--p12.3, and identification of a
 RT polymorphic CA-repeat marker in the OLR1 gene.";
 RL Cytogenet. Cell Genet. 82:34-36(1998).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA], DOMAIN, DISULFIDE BONDS, N-GLYCOSYLATION,
 RP AND MUTAGENESIS OF CYS-144; CYS-155; CYS-172; ASN-183;
 RP 209-ARG-ASN-210; CYS-226; ARG-229; ARG-231; 235-SER-GLN-236; SER-240;
 RP CYS-243; CYS-256; CYS-264 AND 267-LYS--GLN-273.
 RX MEDLINE=21157417; PubMed=11256994;
 RA Shi X., Nimi S., Ohtani T., Machida S.;
 RT "Characterization of residues and sequences of the carbohydrate
 RT recognition domain required for cell surface localization and ligand
 RT binding of human lectin-like oxidized LDL receptor.";
 RL J. Cell Sci. 114:1273-1282(2001).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], TISSUE SPECIFICITY, AND INDUCTION.
 RX MEDLINE=99047525; PubMed=9828121; DOI=10.1006/geno.1998.5561;
 RA Yamanaka S., Zhang X.-Y., Miura K., Kim S., Iwao H.;
 RT "The human gene encoding the lectin-type oxidized LDL receptor (OLR1)
 RT is a novel member of the natural killer gene complex with a unique
 RT expression profile.";
 RL Genomics 54:191-199(1998).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [MRNA], INVOLVEMENT IN MYOCARDIAL INFARCTION, AND
 RP VARIANT ASN-167.
 RX MEDLINE=22533240; PubMed=12646194;
 RA Tatsuguchi M., Furutani M., Hinagata J.-I., Tanaka T., Furutani Y.,
 RA Inamura S.-I., Kawana M., Masaki T., Kasanuki H., Sawamura T.,
 RA Matsuo R.;
 RT "Oxidized LDL receptor gene (OLR1) is associated with the risk of
 RT myocardial infarction.";
 RL Biochem. Biophys. Res. Commun. 303:247-250(2003).
 RN [6]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RX Millar D.S.;
 RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Placenta;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Siemsen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg H., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP FUNCTION
 RX MEDLINE=21679116; PubMed=11821063;
 RA Hayaashida K., Kume N., Minami M., Kita T.;
 RT "Lectin-like oxidized LDL receptor-1 (LOX-1) supports adhesion of
 RT mononuclear leukocytes and a monocyte-like cell line THP-1 cells under
 RT static and flow conditions.";
 RL FEBS Lett. 511:133-138(2002).
 RN [9]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX MEDLINE=22241698; PubMed=12354387;
 RA Delneste Y., Magistrelli G., Gauchat J.-P., Haeuw J.-P., Aubry J.-F.,
 RA Nakamura K., Kawakami-Honda N., Goetsch L., Sawamura T.,
 RA Bonnefoy J.-P., Jeannin P.;
 RT "Involvement of LOX-1 in dendritic cell-mediated antigen cross-
 RT presentation.";
 RL Immunity 17:353-362(2002).
 RN [10]
 RP INVOLVEMENT IN AD DISEASE
 RX PubMed=12384789; DOI=10.1007/s00439-002-0802-7;
 RA Lueddecking-Zimmer E., DeKosky S.T., Chen Q., Barmada M.M.,
 RA Kamboh M.I.;
 RT "Investigation of oxidized LDL-receptor 1 (OLR1) as the candidate gene
 RT for Alzheimer's disease on chromosome 12.";
 RL Hum. Genet. 111:443-451(2002).
 RN [11]
 RP INDUCTION.
 RX MEDLINE=22760283; PubMed=12878212;
 RA Hu B., Li D., Sawamura T., Mehta J.L.;
 RT "Oxidized LDL through LOX-1 modulates LDL-receptor expression in human
 RT coronary artery endothelial cells.";
 RL Biochem. Biophys. Res. Commun. 307:1008-1012(2003).
 RN [12]
 RP INVOLVEMENT IN MYOCARDIAL INFARCTION.
 RX PubMed=12810610; DOI=10.1161/01.CIR.0000074207.85796.36;
 RA Chen Q., Reis S.E., Kammerer C., Craig W.Y., Labierre S.E.,
 RA Zimmer E.L., McNamara D.M., Pauly D.F., Sharaf B., Holubkov R.,
 RA Bairey Merz C.N., Sopko G., Bontempo F., Kamboh M.I.;
 RT "Genetic variation in lectin-like oxidized low-density lipoprotein
 RT receptor 1 (LOX1) gene and the risk of coronary artery disease.";
 RL Circulation 107:3146-3151(2003).
 RN [13]
 RP INVOLVEMENT IN AD DISEASE.
 RX MEDLINE=22692680; PubMed=12807963;
 RA Lambert J.-C., Lueddecking-Zimmer E., Merrot S., Hayes A., Thaker U.,
 RA Desai P., Houzet A., Hermant X., Cottel D., Pritchard A., Iwatsubo T.,
 RA Pasquier F., Frigard B., Conneally P.M., Chartier-Harlin M.-C.,
 RA DeKosky S.T., Lendon C., Mann D., Kamboh M.I., Anouyel P.;
 RT "Association of 3'-UTR polymorphisms of the oxidized LDL receptor 1
 RT (OLR1) gene with Alzheimer's disease.";
 RL J. Med. Genet. 40:424-430(2003).
 RN [14]
 RP HOMODIMERIZATION, INTERCHAIN DISULFIDE BOND, AND MUTAGENESIS OF
 RP CYS-140.
 RX PubMed=15000751; DOI=10.1089/104454904322759920;
 RA Xie Q., Matsunaga S., Nimi S., Ogawa S., Tokuyasu K., Sakakibara Y.,
 RA Machida S.;
 RT "Human lectin-like oxidized low-density lipoprotein receptor-1
 RT functions as a dimer in living cells.";

RL DNA Cell Biol. 23:111-117(2004).
RN [15]
RX LACK OF INVOLVEMENT IN AD DISEASE.
RX PubMed=15060104;
RA Bertram L., Parkinson M., Mullin K., Menon R., Blacker D., Tanzi R.E.;
RT "No association between a previously reported OBR1 3' UTR polymorphism
RL and Alzheimer's disease in a large family sample.";
RN J. Med. Genet. 41:286-288(2004).
RN [16]
RX LACK OF INVOLVEMENT IN AD DISEASE.
RX PubMed=15276231; DOI=10.1016/j.neulet.2004.05.023;
RA Pritchard A., St Clair D., Lemmon H., Mann D.M.A., Lendon C.;
RT "No association between polymorphisms in the lectin-like oxidised low
RT density lipoprotein receptor (ORL1) gene on chromosome 12 and
RT Alzheimer's disease in a UK cohort.";
RN Neurosci. Lett. 366:126-129(2004).
RN [17]
RX INVOLVEMENT IN MYOCARDIAL INFARCTION.
RX PubMed=15976314; DOI=10.1161/01.RES.0000174563.62625.8e;
RA Mango R., Biocca S., Del Vecchio F., Clementi F., Sangiulio F.,
RA Amati F., Filaretto A., Girelli S., Spitalieri P., Filesi I.,
RA Favalli C., Lauro R., Mehta J.L., Romeo F., Novelli G.;
RT "In vivo and in vitro studies support that a new splicing isoform of
RT ORL1 gene is protective against acute myocardial infarction.";
RN Circ. Res. 0:0-0(2005).
RN [18]
RX INVOLVEMENT IN AD DISEASE.
RX PubMed=15860461;
RA D'Introno A., Solfrizzi V., Colacicco A.M., Capurso C., Torres F.,
RA Capurso S.A., Capurso A., Panza F.;
RT "Polymorphisms in the oxidized low-density lipoprotein receptor-1 gene
RT and risk of Alzheimer's disease.";
RN J. Gerontol. 60:280-284(2005).
RN [19]
RX DOMAIN, SUBCELLULAR LOCATION, AND MUTAGENESIS OF 22-LYS--LYS-25 AND
RX GLU-70.
RX PubMed=15935375; DOI=10.1016/j.yjmcc.2005.05.001;
RA Chen M., Sawamura T.;
RT "Essential role of cytoplasmic sequences for cell-surface sorting of
RT the lectin-like oxidized LDL receptor-1 (LOX-1).";
RN J. Mol. Cell. Cardiol. 0:0-0(2005).
RN [20]
RX X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 136-270, SUBUNIT, AND
RX DISULFIDE BONDS.
RX PubMed=15695803; DOI=10.1074/jbc.M500768200;
RA Park H., Adait F.G., Boyington J.C.;
RT "The 1.4 anstrom crystal structure of the human oxidized low density
RT lipoprotein receptor lox-1.";
RN J. Biol. Chem. 280:13593-13599(2005).
RN [21]
RX X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 143-271, SUBUNIT, DISULFIDE
RX BONDS, AND MUTAGENESIS OF TRP-150; ARG-208; ARG-209; HIS-226; ARG-229;
RX ARG-231 AND ARG-248.

Query Match 39.4%; Score 52; DB 1; Length 273;
Best Local Similarity 36.4%; Pred. No. 17;
Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 2 LHNQEVTAEDGTQRAEKCSKPC 23
DB 123 LHHQNLQETLKRVCNSAPC 144
|||: : : : :
|||: : : : :

RESULT 12
Q7S109_NEUCR
ID Q7S109_NEUCR PRELIMINARY; PRT; 498 AA.
AC Q7S109;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU07762.1;
OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krytofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Piamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000470; EAA29020.1; -; Genomic_DNA.
DR InterPro; IPR003014; PAN.
DR Pfam; PF00024; PAN; 1.
KW Hypothetical protein.
SQ SEQUENCE 498 AA; 56281 MW; 468DFD06F34E22D7 CRC64;

Query Match 38.6%; Score 51; DB 2; Length 498;
Best Local Similarity 44.4%; Pred. No. 46;
Matches 8; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 EVTAEDGTQRAEKCSKPC 23
DB 435 EVAVVEGVGEKARECGKCC 452
|||: : : : :
|||: : : : :

RESULT 13
Q4QG99_LEIMA
ID Q4QG99_LEIMA PRELIMINARY; PRT; 670 AA.
AC Q4QG99;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=LmjF13.0550;
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Friedlin;
RA Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA Saunders D., Seeger K., Warren T., Apostolou Z., Bauser C., Beck A.,
RA Bianchetti G., Borzym K., Bothe G., Bruschi C., Carloni L.,
RA Duesterhoeft A., Fuchs M., Gabel C., Goffeau A., Hilbert H.,
RA Klages S., Kube M., Marra M., Masuy D., Mueller-Auer S., Fohl T.,
RA Purnelle B., Reinhardt R., Rieger M., Robben J., Schaefer M.,
RA Tosato V., Volckaert G., Wambutt R., Wedler H., Zimmermann M.,
RA Rajandream M., and Barrell B.G.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CT005252; CAJ02599.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 670 AA; 71637 MW; 65BE3208BE5C544 CRC64;

Query Match 38.3%; Score 50.5; DB 2; Length 670;
Best Local Similarity 41.4%; Pred. No. 76;
Matches 12; Conservative 3; Mismatches 5; Indels 9; Gaps 1;


```

DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR InterPro; IPR006211; Furin-like.
DR Pfam; PF00757; Furin-like; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 74
SQ SEQUENCE 74 AA; 8155 MW; B3BEF7953BBCOAE CRC64;

Query Match 37.1%; Score 49; DB 2; Length 74;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 10 EDGQRAEKCKSPC 23
Db 31 EDGVRCKCKCGPC 44

RESULT 19
Q9BG67_RABIT PRELIMINARY; PRT; 116 AA.
AC Q9BG67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor tyrosine kinase ErbB1 (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

NUCLEOTIDE SEQUENCE.
RA Klonisch T., Wolf P., Hombach-Klonisch S., Vogt S., Kuechenhoff A.,
RA Tetens F., Fischer B.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333177; AAK14370.1; -; mRNA.
DR HSP; Q9H2C9; IMOX.
DR SMR; Q9BG67; 1-113.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . . ; IEA.
DR InterPro; IPR006211; Furin-like.
DR Pfam; PF00757; Furin-like; 1.
DR Kinase; Receptor.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12624 MW; 6561F79C0FF2322F CRC64;

Query Match 37.1%; Score 49; DB 2; Length 116;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 10 EDGQRAEKCKSPC 23
Db 42 EDGVRCKCKCGPC 55

RESULT 20
VXIS_BPSF5
ID VXIS_BPSF5 STANDARD; PRT; 147 AA.
AC Q2010;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Excisionase.

```

```

GN Name=XIS; Synonyms=27;
OC Bacteriophage SFV (Shigella flexneri bacteriophage V).
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=55884;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97449297; PubMed=9305766; DOI=10.1016/S0378-1119(97)00144-3;
RA Huan P.T., Whittle B.L., Bastin D.A., Lindberg A.A., Verma N.K.;
RT "Shigella flexneri type-specific antigen V: cloning, sequencing and
RT characterization of the glucosyl transferase gene of temperate
RT bacteriophage SFV.";
RL Gene 195:207-216(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=21886391; PubMed=11889106;
RX DOI=10.1128/JB.184.7.1974-1987.2002;
RA Allison G.E., Angeles D., Tran-Binh N., Verma N.K.;
RT "Complete genomic sequence of SFV, a serotype-converting temperate
RT bacteriophage of Shigella flexneri.";
RL J. Bacteriol. 184:1974-1987(2002).
CC -|- FUNCTION: Excisionase and integrase are necessary for the excision
CC of prophage from the host genome by site-specific recombination
CC (by similarity).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U82619; AAB72136.1; -; Genomic_DNA.
CC DNA recombination; DNA-binding.
CC SEQUENCE 147 AA; 16524 MW; 37A541BBBABC08F7 CRC64;

Query Match 37.1%; Score 49; DB 1; Length 147;
Best Local Similarity 47.4%; Pred. No. 26;
Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 PLHNQEVTAEDGTQRAEKC 19
Db 90 PLHTVQVSAGDGITEERKC 108

RESULT 21
Q68GS5_HUMAN PRELIMINARY; PRT; 405 AA.
AC Q68GS5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Epidermal growth factor receptor short isoform.
GN Name=EGFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Xu L., Hong A., He X.;
RT "Cloning of the cDNA for a short EGF receptor from human placenta.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY698024; AAT97979.1; -; mRNA.
DR Receptor.
SQ SEQUENCE 405 AA; 44664 MW; F5DEB31787EF1822 CRC64;

Query Match 37.1%; Score 49; DB 2; Length 405;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 10 EDGQRAEKCKSPC 23
Db 320 EDGVRCKCKCGPC 333

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RT "None Title.";
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB209442; BAD92679.1; -; mRNA.
DR SMR; Q59FL8; 25-509.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006119; F:electron transport; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro; IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00757; Furin-like; 1.
DR PRINTS; PR01030; Recep_L_domain; 1.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR SMART; SM00261; FU; 3.
DR SMART; SM00220; S_Tkc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor.
FT NON_TER 1
SQ SEQUENCE 1081 AA; 119952 MW; C3BAF46C211A86DC CRC64;

Query Match 37.1%; Score 49; DB 2; Length 1081;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 10 EDGTORAEKCKSPC 23
    ||| : : : |||
Db 191 EDGVRKCKCEGPC 204

RESULT 24
Q504U8 HUMAN
ID Q504U8_HUMAN PRELIMINARY; PRT; 1091 AA.
AC Q504U8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE EGFR protein.
GN Name=EGFR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustun T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC094761; AAH94761.1; -, mRNA.
DR SMR: Q504U8; 26-593.
DR InterPro: IPR001450; 4Fe4S_Fe_S_bd.
DR InterPro: IPR000494; EGFR_L.
DR InterPro: IPR006211; Furin-like.
DR InterPro: IPR006212; Furin repeat.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002290; Ser_Thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR008266; Tyr_pkinase_AS.
DR Pfam: PF01030; Recep_L domain; 2.
DR PRINTS: PR00353; 4FE4SERDOXIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00261; FU; 3.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
SQ SEQUENCE 1091 AA; 120692 MW; 25B062C735D62AD1 CRC64;
Query Match 37.1%; Score 49; DB 2; Length 1091;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 10 EDGTQRAEKCKGPC 23
DB 275 EDGVRKCKCEGPC 288
|||||:::|||||
RESULT 25
ID Q8MIL8_PIG PRELIMINARY; PRT; 1209 AA.
AC Q8MIL8_2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epidermal growth factor receptor.
OS Sus scrofa (pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kim J.G., Vallet J.L., Nonnenan D., Christenson R.K.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY117054; AAH74742.1; -, mRNA.
DR HSP; Q9H2C9; 1M17.
DR SMR: Q8MIL8; 25-525, 27-636.
DR GO: GO:0016020; C:membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0005006; F:epidermal growth factor receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO: GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.

DR InterPro: IPR000494; EGFR_L.
DR InterPro: IPR006211; Furin-like.
DR InterPro: IPR006212; Furin repeat.
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR008266; Tyr_pkinase_AS.
DR Pfam: PF01030; Recep_L domain; 2.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00261; FU; 5.
DR SMART: SM00219; TyKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW Receptor.
SQ SEQUENCE 1209 AA; 133531 MW; 268E3FB11E36F90F CRC64;
Query Match 37.1%; Score 49; DB 2; Length 1209;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 10 EDGTQRAEKCKGPC 23
DB 320 EDGVRKCKCEGPC 333
|||||:::|||||
RESULT 26
ID EGFR_HUMAN STANDARD; PRT; 1210 AA.
AC P00533; Q00688; Q00732; P06268; Q14225; Q92795; Q9BZS2; Q9GZX1;
AC Q9H2C9; Q9H3C9; Q9UMD7; Q9UMD8; Q9UMG5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor
DE tyrosine-protein kinase ErbB-1).
GN Name=EGFR; Synonyms=ERBB1;
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE (ISOFORM 1).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Varden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayes E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
RT "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells";
RL Nature 309:418-425 (1984).
RN [2]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=95382957; PubMed=7654368; DOI=10.1262/jrd.41.149;
RA Ilekis J.V., Stark B.C., Scoccia B.;
RT "Possible role of variant RNA transcripts in the regulation of
RT epidermal growth factor receptor expression in human placenta";
RL Mol. Reprod. Dev. 41:149-156 (1995).
RN [3]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=97078686; PubMed=8918811; DOI=10.1093/nar/24.20.4050;
RA Reiter J.L., Mailhe N.J.;
RT "A 1.8 kb alternative transcript from the human epidermal growth
RT factor receptor gene encodes a truncated form of the receptor";
RL Nucleic Acids Res. 24:4050-4056 (1996).
RN [4]
RP NUCLEOTIDE SEQUENCE (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=97256547; PubMed=9103388; DOI=10.1006/gyno.1996.4526;
RA Ilekis J.V., Gariti J., Niederberger C., Scoccia B.;

RT "Expression of a truncated epidermal growth factor receptor-like
RT protein (TEGFR) in ovarian cancer.";
RN Genocol. Oncol. 65:36-41(1997).
RN [5]
RC TISSUE=Placenta;
RX MEDLINE=21100872; PubMed=11161793; DOI=10.1006/geno.2000.6341;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
RA Maihle N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative EGFR transcripts encoding truncated receptor
RT isoforms.";
RN Genomics 71:1-20(2001).
RN [6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS GLN-98; ARG-266;
RP LYS-521; ILE-674; GLY-962 AND PRO-988.
RA Livingstone R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.;
RT "NIHNS SNPs, environmental genome project. NIHNS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE OF 575-687.
RA Reiter J.L., Threadgill D.W., Danielsen A.J., Schehl C.M.,
RA Lampland A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
RA Maihle N.J.;
RT "Human and mouse alternative EGFR transcripts encoding only the
RT extracellular domain of the receptor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP NUCLEOTIDE SEQUENCE OF 713-924.
RX MEDLINE=84196372; PubMed=6326261;
RA Lin C.R., Chen W.S., Krutiger W.; Stolarsky L.S., Weber W., Evans R.M.,
RA Verma I.M., Gill G.N., Rosenfeld M.G.;
RT "Expression cloning of human EGF receptor complementary DNA: gene
RT amplification and three related messenger RNA products in A431
RT cells.";
RL Science 224:843-848(1984).
RN [9]
RN NUCLEOTIDE SEQUENCE OF 150-962.
RX MEDLINE=84245835; PubMed=6330563;
RA Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
RA Roe B.A., Merlino G.T., Pastan I.;
RT "Human epidermal growth factor receptor cDNA is homologous to a
RT variety of RNAs overproduced in A431 carcinoma cells.";
RL Nature 309:806-810(1984).
RN [10]
RP NUCLEOTIDE SEQUENCE OF 1028-1210.
RX MEDLINE=85046483; PubMed=6093780;
RA Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
RA O'Malley B.W.;
RT "Isolation of an evolutionarily conserved epidermal growth factor
RT receptor cDNA from human A431 carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 124:125-132(1984).
RN [11]
RP NUCLEOTIDE SEQUENCE OF 1-29.
RX MEDLINE=88217333; PubMed=3329716;
RA Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
RA Waterfield M.D.;
RT "The human EGF receptor gene: structure of the 110 kb locus and
RT identification of sequences regulating its transcription.";
RL Oncogene Res. 1:375-396(1987).
RN [12]
RP NUCLEOTIDE SEQUENCE OF 1-29.
RX MEDLINE=91107677; PubMed=1988448;
RA Haley J.D., Waterfield M.D.;
RT "Contributory effects of de novo transcription and premature
RT transcript termination in the regulation of human epidermal growth
RT factor receptor proto-oncogene RNA synthesis.";
RL J. Biol. Chem. 266:1746-1753(1991).
RN [13]
RN NUCLEOTIDE SEQUENCE OF 1-29.
RX MEDLINE=85270438; PubMed=2991899;
RA Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
RT "Characterization and sequence of the promoter region of the human
RT epidermal growth factor receptor gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924(1985).
RN [14]
RN NUCLEOTIDE SEQUENCE OF 25-49.
RX MEDLINE=84172183; PubMed=6324343;
RA Weber W., Gill G.N., Spiess J.;
RT "Production of an epidermal growth factor receptor-related protein.";
RL Science 224:294-297(1984).
RN [15]
RP PROTEIN SEQUENCE OF 540.
RA Kohda D.;
RL Submitted (SEP-1997) to Swiss-Prot.
RN [16]
RP PROTEIN SEQUENCE OF 687-705; 986-998; 1000-1023; 1026-1030 AND
RP 1068-1077, AND PHOSPHORYLATION SITES THR-693; SER-695; SER-1070 AND
RP SER-1071.
RX MEDLINE=88330814; PubMed=3138233;
RA Heisermann G.J., Gill G.N.;
RT "Epidermal growth factor receptor threonine and serine residues
RT phosphorylated in vivo.";
RL J. Biol. Chem. 263:13152-13158(1988).
RN [17]
RP PROTEIN SEQUENCE OF 25-39.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Hensel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Protein Sci. 13:2819-2824(2004).
RN [18]
RP PROTEIN SEQUENCE OF 740-744 AND 746-747.
RX MEDLINE=85182850; PubMed=2985580;
RA Russo M.W., Lukas T.J., Cohen S., Staros J.V.;
RT "Identification of residues in the nucleotide binding site of the
RT epidermal growth factor receptor/kinase.";
RL J. Biol. Chem. 260:5205-5208(1985).
RN [19]
RN RECEPTOR ACTIVITY.
RX MEDLINE=84191554; PubMed=6325948;
RA Mroczkowski B., Mosig G., Cohen S.;
RT "ATP-stimulated interaction between epidermal growth factor receptor
RT and supercoiled DNA.";
RL Nature 309:270-273(1984).
RN [20]
RP LIGAND BINDING.
RX MEDLINE=90003233; PubMed=2790960; DOI=10.1016/0092-8674(89)90867-2;
RA Chen W.S., Lazar C.S., Lund K.A., Welsh J.B., Chang C.P., Walton G.M.,
RA Der C.J., Wiley H.S., Gill G.N., Rosenfeld M.G.;
RT "Functional independence of the epidermal growth factor receptor from
RT a domain required for ligand-induced internalization and calcium
RT regulation.";
RL Cell 59:33-43(1989).
RN [21]
RP PHOSPHORYLATION.
RX MEDLINE=89278137; PubMed=2543678;
RA Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
RA Hawk R., Givol D., Ullrich A., Schlessinger J.;
RT "All autophosphorylation sites of epidermal growth factor (EGF)
RT receptor and HER2/neu are located in their carboxyl-terminal tails.
RT Identification of a novel site in EGF receptor.";
RL J. Biol. Chem. 264:10667-10671(1989).
RN [22]
RP CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444 AND
RP ASN-528.
RX MEDLINE=96398132; PubMed=8962717;
RA Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
RT "Analysis of the glycosylation patterns of the extracellular domain of
RT the epidermal growth factor receptor expressed in Chinese hamster
RT ovary fibroblasts.";

RESULT 29	
Q6JQ08_LATME	
ID	Q6JQ08 LATME PRELIMINARY; PRT; 514 AA.
AC	Q6JQ08;
DT	05-JUL-2004 (T=EMBLrel. 27, Created)
DT	05-JUL-2004 (T=EMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (T=EMBLrel. 27, Last annotation update)
DE	Rag-1 (Fragment).
OS	Lutimaria menadoensis (Indonesian coelacanth).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;


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RA Pellenberg K., Boutros M., Vingron M., Sauer F., Hoheisel J.D.,
RA Paro R.;
RT "An integrated gene annotation and transcriptional profiling approach
RL towards the full gene content of the Drosophila genome.";
RL Genome Biol. 5:RESEARCH0003.1-RESEARCH0003.17(2003)).
CC -I- MISCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB third party annotation (TPA) entry.
DR EMBL; BK003679; DAA02377.1; -; Genomic DNA.
SQ SEQUENCE 150 AA; 16067 MW; 5657862531B2DD35 CRC64;

Query Match 36.4%; Score 48; DB 2; Length 150;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 10; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 QEVTAEDGTQRAEKCSPCA 24
DB 25 QCMVEMGTSFAERCSQPA 44

RESULT 33
O8XDI3 EC057 PRELIMINARY; PRT; 214 AA.
AC O8XDI3; 07AEV8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE complete genome (Hypothetical protein ECs1696).
GN OrderedLocusNames=ECs1696, z1963;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074933; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G., Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Godbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouais K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RT Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005174; AAC56051.1; -; Genomic DNA.
DR EMBL; BA000007; BAB35119.1; -; Genomic DNA.
DR PIR; G85698; G85698.
DR PIR; H90840; H90840.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000051; SAM bind.
KW Complete proteome; Hypothetical protein; Methyltransferase;
KW Transferase
SQ SEQUENCE 214 AA; 23967 MW; 229CAF9C77704BE0 CRC64;

Query Match 36.4%; Score 48; DB 2; Length 214;
Best Local Similarity 45.5%; Pred. No. 55;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 3 HNOEVTAEADGTQRAEKCSPCA 24
DB 20 HRTEKTPDHWQRAEKMAENCA 41

RESULT 35
O87503 ECOLI PRELIMINARY; PRT; 270 AA.
AC O87503;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orf2.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFT073;
RX MEDLINE=97342757; PubMed=9199454;
SQ SEQUENCE 269 AA; 30722 MW; D5352DAAFC1D745C CRC64;

Query Match 36.4%; Score 48; DB 2; Length 269;
Best Local Similarity 45.5%; Pred. No. 70;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 3 HNOEVTAEADGTQRAEKCSPCA 24
DB 20 HRTEKTPDHWQRAEKMAENCA 41

RESULT 34
O83LE8 SHIFL PRELIMINARY; PRT; 269 AA.
AC O83LE8; 07C122;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=Sl277, SF1191;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RA "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G., Rose D.J., Barling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RA "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).
DR EMBL; AE005674; AAN42805.1; -; Genomic DNA.
DR EMBL; AS015982; AAP16693.1; -; Genomic DNA.
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransferase; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000051; SAM bind.
KW Complete proteome; Hypothetical protein; Methyltransferase;
KW Transferase
SQ SEQUENCE 269 AA; 30722 MW; D5352DAAFC1D745C CRC64;

Query Match 36.4%; Score 48; DB 2; Length 269;
Best Local Similarity 45.5%; Pred. No. 70;
Matches 10; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
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RESULT 37	
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AC Q9ESE0;	PRT; 478 AA.
DT 01-MAR-2001	(TrEMBLrel. 16. Created)

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RESULT 38
ID Q6NKT4 ARATH PRELIMINARY; PRT; 632 AA.
OC GNKT4;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE AL4g14650.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
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OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL "Arabidopsis ORF clones.";
RT Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BT012609; AAT06428.1; -; mRNA.
DR EMBL; BT020594; AAW80867.1; -; mRNA.
SQ SEQUENCE 632 AA; 70003 MW; 08F4F98935AA639B CRC64;

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Db 393 VHDEVTDKGADKAISNKPFS 415

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Epidermal growth factor receptor isoform 2.
GN Name=Egfr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/101;
RX MEDLINE=21100872; PubMed=11161793; DOI=10.1006/geno.2000.6341;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Schehl Sinclair C., Pearsall R.S., Green P.J., Yee D., Lampland A.L.,
RA Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
RA Maibhe N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative EGFR transcripts encoding truncated receptor
RT isoforms";
RL Genomics 71.1-20(2001).
DR EMBL; AF275366; AAC28046.1; -; Genomic_DNA.
DR EMBL; AF275364; AAC28046.1; JOINED; Genomic_DNA.
DR EMBL; AF275365; AAC28046.1; JOINED; Genomic_DNA.
DR HSSP; O9H2C9; IMOX.
DR SMR; QSERV6; 27-631.
DR MGI; MGI:95294; Egfr.
DR GO; GO:0016323; C:basolateral plasma membrane; IDA.
DR GO; GO:0030139; C:endocytic vesicle; IDA.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005622; C:intracellular; IDA.
DR GO; GO:0016301; F:kinase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004871; F:signal transducer activity; IDA.
DR GO; GO:0050730; P:regulation of peptidyl-tyrosine phosphoryla. .; IMP.
DR GO; GO:0007165; P:signal transduction; IDA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000494; EGFR_L.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin_repeat.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF01030; Recep_L domain; 2.
DR PRINTS; PR00353; 4FE4SFERDOXIN.
DR SMART; SM00261; FU; 3.
KW Receptor.
SQ SEQUENCE 643 AA; 71476 MW; DEF22002C84911B1 CRC64;

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Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 10 EDCQRAEKCKPCA 23
Db 320 EDGIRKCKCDGPC 333

RESULT 40
O23321_ARATH
ID O23321_ARATH PRELIMINARY; PRT; 644 AA.

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O23321;
AC 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein dl3365c (Hypothetical protein AT4g14650).
GN Name=dl3365c; Synonym=AT4g14650;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bavan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Estian K.D., Rieger M., James R.,
RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Ansoorge W., Delsey M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalwatizis N.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97336; CAB10244.1; -; Genomic_DNA.
DR EMBL; AL161539; CAB78507.1; -; Genomic_DNA.
DR PIR; B71409; B71409.
KW Hypothetical protein.
SQ SEQUENCE 644 AA; 71277 MW; 8057168456922960 CRC64;

Query Match      36.4%; Score 48; DB 2; Length 644;
Best Local Similarity 39.1%; Pred. No. 1.8e+02;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 2 LHNQEVTAEDGTQRAEKCKPCA 24
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Job time : 167.273 secs

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GenCore version 5.1.6
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OM' protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 22:22:28 ; Search time 2200.91 Seconds
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Title: US-09-632-036f-6

Perfect score: 132

Sequence: 1 PLHQEVTAEDGTQAEKCKPCA 24

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	97.0	471	6	AX379026 Sequence
2	128	97.0	1219	6	CS085264 Sequence
3	128	97.0	1316	8	AF177761 Homo sapi

CS075259 Sequence	1320	97.0	6	CS075259
CS085263 Sequence	1459	97.0	6	CS085263
CS085262 Sequence	1699	97.0	6	CS085262
AR181000 Sequence	1872	97.0	6	AR181000
CS085261 Sequence	1939	97.0	6	CS085261
CS075237 Sequence	1944	97.0	6	CS075237
CS020247 Sequence	2028	97.0	6	CS020247
CS020248 Sequence	2028	97.0	6	CS020248
CS075249 Sequence	2061	97.0	6	CS075249
CS085268 Sequence	2086	97.0	6	CS085268
CS085269 Sequence	2086	97.0	6	CS085269
CS085270 Sequence	2086	97.0	6	CS085270
CS085271 Sequence	2086	97.0	6	CS085271
CS075235 Sequence	2320	97.0	6	CS075235
AR082744 Sequence	2385	97.0	6	AR082744
AR099963 Sequence	2385	97.0	6	AR099963
AR143949 Sequence	2385	97.0	6	AR143949
CS075247 Sequence	2437	97.0	6	CS075247
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AX023363 Sequence	2871	97.0	6	AX023363
AX505114 Sequence	3678	97.0	6	AX505114
AR034479 Sequence	3768	97.0	6	AR034479
BD224136 Novel met	3768	97.0	6	BD224136
BD267514 HER-2/neu	3768	97.0	6	BD267514
CQ815384 Sequence	3768	97.0	6	CQ815384
CQ841302 Sequence	3768	97.0	6	CQ841302
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82 128 97.0 9274 6 AX060703 Sequence
83 128 97.0 30837 8 AY208911 Homo sapi
84 128 97.0 89963 8 CR626867 Human DNA
85 128 97.0 151284 8 CR626880 Human DNA
86 128 97.0 154278 14 AC025531 Homo sapi
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88 128 97.0 161815 8 AC079199 Homo sapi
89 128 97.0 168585 8 AC040933 Homo sapi
90 128 97.0 198008 14 AC142197 Homo sapi
91 121 91.7 3780 4 AB008451 Canis fam
92 121 91.7 3783 4 AY702651 Felis cat
93 114 86.4 641 10 BV070407 Homo sapi
94 114 86.4 2083 6 CS085260 Sequence
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ALIGNMENTS

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DEFINITION Sequence 68 from Patent WO0196389.
ACCESSION AX379026
VERSION AX379026.1 GI:19574866
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Meagher,M.J., King,G.E., Xu,J. and Secrist,H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer
JOURNAL Patent: WO 0196389-A 68 20-DEC-2001;
CORIXA CORPORATION (US)
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Query Match: 96.97% Indels: 0
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US-09-632-036F-6 (1-24) x AX379026 (1-471)
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RESULT 2
CS085264
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LOCUS CS085264 1219 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 6 from Patent WO2005039618.
ACCESSION CS085264
VERSION CS085264.1 GI:66711221
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu -encoding DNA and therapeutic uses thereof
JOURNAL Patent: WO 2005039618-A 6 06-MAY-2005;
Indena S.p.A. (IT)
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QY 21 LysProCysAla 24
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Db 170 AAGCCCTGTGCC 181
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LOCUS AF177761 1316 bp mRNA linear PRI 20-SEP-2000
DEFINITION Homo sapiens herstatin (HER-2) mRNA, alternatively spliced,
complete cds.
ACCESSION AF177761
VERSION AF177761.2 GI:10181232
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1316)
AUTHORS Doherty,J.K., Bond,C., Jardim,A., Adelman,J.P. and Clinton,G.M.
TITLE The HER-2/neu receptor tyrosine kinase gene encodes a secreted
autoinhibitor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (19), 10869-10874 (1999)
PUBMED 10485918
REFERENCE 2 (bases 1 to 1316)
AUTHORS Doherty,J.K., Clinton,G.M. and Adelman,J.P.
TITLE Direct Submission
JOURNAL Submitted (16-AUG-1999) Biochemistry, Oregon Health Sciences
University, 3181 SW Sam Jackson Park Road, Portland, OR 97201, USA
REFERENCE 3 (bases 1 to 1316)
AUTHORS Doherty,J.K., Clinton,G.M., Adelman,J.P., Evans,A.J. and
Henner,W.D.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2000) Biochemistry, Oregon Health Sciences
University, 3181 SW Sam Jackson Park Road, Portland, OR 97201, USA
REMARK Sequence update by submitter
COMMENT On Sep 18, 2000 this sequence version replaced gi:5917723.
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Score: 128.00 Matches: 23
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Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
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Qy 21 LysProCysAla 24
Db 650 AAGCCCTGTGCC 661

RESULT 7
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LOCUS AR181000 1872 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6333169.
ACCESSION AR181000
VERSION AR181000.1 GI:20223033
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1872)
AUTHORS Hudziak,R.Michael., Shepard,H.Michael. and Ullrich,A.
TITLE HER2 extracellular domain
JOURNAL Patent: US 6333169-A 2 25-DEC-2001;
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Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US 09-632-036F-6 (1-24) x AR181000 (1-1872)

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Qy 21 LysProCysAla 24
Db 943 AAGCCCTGTGCC 954

RESULT 8
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LOCUS CS085261 1939 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 3 from Patent WO2005039618.
ACCESSION CS085261
VERSION CS085261.1 GI:66711218
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1

AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE Pl85 sp neu /sp -encoding DNA and Therapeutical uses thereof
JOURNAL Patent: WO 2005039618-A 3 06-MAY-2005;
Indena S.p.A. (IT)
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Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 1..91e-10 Length: 1939
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS085261 (1-1939)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 830 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACGCGGTGTGAGAAGTGCAGC 889

Qy 21 LysProCysAla 24
Db 890 AAGCCCTGTGCC 901

RESULT 9
CS075237
LOCUS CS075237 1944 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 3 from Patent WO2005033133.
ACCESSION CS075237
VERSION CS075237.1 GI:63091609
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shemesh,R., Oren,A., Rotman,G., Sela-Tavor,O., Walach,S., Sameach-Greenwald,S., Beiman,M., Eshel,D. and Savitsky,K.
TITLE Polynucleotides encoding novel ErbB-2 polypeptides and kits and methods using same
JOURNAL Patent: WO 2005033133-A 3 14-APR-2005;
Compugen Ltd. (IL)
FEATURES
Location/Qualifiers
source
1..1944
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1..91e-10 Length: 1944
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS075237 (1-1944)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACGCGGTGTGAGAAGTGCAGC 1155

Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167
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RESULT 10
CS020247
LOCUS      CS020247      2028 bp      DNA      linear      PAT 23-FEB-2005
DEFINITION Sequence 9 from Patent WO2005012527.
ACCESSION CS020247
VERSION   CS020247.1 GI:60220905
KEYWORDS  synthetic construct
SOURCE    other sequences; artificial sequences.
ORGANISM  1
REFERENCE Gallo,P.I., Monaci,P.I. and Nuzzo,M.I.
AUTHORS   Synthetic gene encoding human epidermal growth factor 2/neu antigen
TITLE     and uses thereof
JOURNAL   Patent: WO 2005012527-A 9 10-FEB-2005;
          Istituto di Ricerche di Biologia Molecolare P. Angeletti S.P.A.
          (IT)
FEATURES
source    Location/Qualifiers
1..2028
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="HER2ECDTwt"
ORIGIN
Alignment Scores:
Pred. No.: 2e-10      Length: 2028
Score: 128.00        Matches: 23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%    Mismatches: 1
Query Match: 96.97%      Indels: 0
DB: 6                Gaps: 0
US-09-632-036F-6 (1-24) x CS020247 (1-2028)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCACAAACAGAGGTGACCGCGAGGACGCCACCCAGCGCTCGAGAGTGCAGC 1005
QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 12
LOCUS      CS075249      2061 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION Sequence 15 from Patent WO2005033133.
ACCESSION CS075249
VERSION   CS075249.1 GI:63091615
KEYWORDS  Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
TITLE     Shemesh,R., Oren,A., Rotman,G., Sela-Tavor,O., Walach,S.,
          Sameach-Greenwald,S., Beiman,M., Eshel,D. and Savitsky,K.
JOURNAL   Polynucleotides encoding novel ErbB-2 polypeptides and kits and
          methods using same
          Patent: WO 2005033133-A 15 14-APR-2005;
          Compugen Ltd. (IL)
FEATURES
source    Location/Qualifiers
1..2061
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2.03e-10   Length: 2061
Score: 128.00        Matches: 23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%    Mismatches: 1
Query Match: 96.97%      Indels: 0
DB: 6                Gaps: 0
US-09-632-036F-6 (1-24) x CS075249 (1-2061)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACAGAGGTGACAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGC 1155
QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167
RESULT 13
LOCUS      CS085268      2086 bp      DNA      linear      PAT 25-MAY-2005
DEFINITION Sequence 10 from Patent WO2005039618.
ACCESSION CS085268
VERSION   CS085268.1 GI:66711225
KEYWORDS  unidentified
SOURCE    unidentified
ORGANISM  unidentified
REFERENCE 1
AUTHORS   Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE     Pl85 sp neu /sp -encoding DNA and therapeutical uses thereof
JOURNAL   Patent: WO 2005039618-A 10 06-MAY-2005;
          Indena S.p.A. (IT)
FEATURES
source    Location/Qualifiers
1..2086
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="HER2ECDTwt"
ORIGIN
Alignment Scores:
Pred. No.: 2e-10      Length: 2086
Score: 128.00        Matches: 23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%    Mismatches: 1
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source
1. .2086
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS085268 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1036

QY 21 LysProCysAla 24
Db 1037 AAGCCCTGTGCC 1048

RESULT 14
LOCUS CS085269 2086 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 11 from Patent WO2005039618.
ACCESSION CS085269
VERSION CS085269.1 GI:66711226
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu /sp -encoding DNA and therapeutic uses thereof
JOURNAL Patent: WO 2005039618-A 11 06-MAY-2005;
Indena S.p.A. (IT)

FEATURES
source
1. .2086
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS085269 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1036

QY 21 LysProCysAla 24
Db 1037 AAGCCCTGTGCC 1048

RESULT 15
LOCUS CS085270 2086 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 12 from Patent WO2005039618.
ACCESSION CS085270
VERSION CS085270.1 GI:66711227
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu /sp -encoding DNA and therapeutic uses thereof
JOURNAL Patent: WO 2005039618-A 13 06-MAY-2005;
Indena S.p.A. (IT)

FEATURES
source
1. .2086
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS085271 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1036

QY 21 LysProCysAla 24
Db 1037 AAGCCCTGTGCC 1048

RESULT 16
LOCUS CS085271 2086 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 13 from Patent WO2005039618.
ACCESSION CS085271
VERSION CS085271.1 GI:66711228
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu /sp -encoding DNA and therapeutic uses thereof
JOURNAL Patent: WO 2005039618-A 13 06-MAY-2005;
Indena S.p.A. (IT)

FEATURES
source
1. .2086
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 2.06e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS085271 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1036

QY 21 LysProCysAla 24
Db 1037 AAGCCCTGTGCC 1048

RESULT 17
LOCUS CS075235
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LOCUS CS075235 2320 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 1 from Patent WO200503133.
ACCESSION CS075235
VERSION CS075235.1 GI:63091608
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Shemesh,R., Oren,A., Rotman,G., Sela-Tavor,O., Walach,S.,
Sameah-Greenwald,S., Beiman,M., Eshel,D. and Savitsky,K.
TITLE Polynucleotides encoding novel ErbB-2 polypeptides and kits and
methods using same
JOURNAL Patent: WO 200503133-A 1 14-APR-2005;
Compugen Ltd. (IL)
FEATURES
source Location/Qualifiers
1..2320
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 2,3e-10 Length: 2320
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
US-09-632-036F-6 (1-24) x CS075235 (1-2320)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155
QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167
RESULT 18
LOCUS AR082744 2385 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 3 from patent US 5976546.
ACCESSION AR082744
VERSION AR082744.1 GI:10009534
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2385)
AUTHORS Laus,R., Ruegg,C.Landon. and Wu,H.
TITLE Immunostimulatory compositions
JOURNAL Patent: US 5976546-A 3 02-NOV-1999;
FEATURES
source Location/Qualifiers
1..2385
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,37e-10 Length: 2385
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
US-09-632-036F-6 (1-24) x AR082744 (1-2385)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

Db 956 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1015
QY 21 LysProCysAla 24
Db 1016 AAGCCCTGTGCC 1027
RESULT 19
LOCUS AR099963 2385 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6080409.
ACCESSION AR099963
VERSION AR099963.1 GI:12810411
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2385)
AUTHORS Laus,R., Ruegg,C.Landon. and Wu,H.
TITLE Immunostimulatory method
JOURNAL Patent: US 6080409-A 3 27-JUN-2000;
FEATURES
source Location/Qualifiers
1..2385
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,37e-10 Length: 2385
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
US-09-632-036F-6 (1-24) x AR099963 (1-2385)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 956 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1015
QY 21 LysProCysAla 24
Db 1016 AAGCCCTGTGCC 1027
RESULT 20
LOCUS AR143949 2385 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 3 from patent US 6210662.
ACCESSION AR143949
VERSION AR143949.1 GI:15105816
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2385)
AUTHORS Laus,R., Ruegg,C.Landon. and Wu,H.
TITLE Immunostimulatory composition
JOURNAL Patent: US 6210662-A 3 03-APR-2001;
FEATURES
source Location/Qualifiers
1..2385
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2,37e-10 Length: 2385
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

RGTLQFEDNYALAVLDNGDPLNNNTTPTVTGASPGGLRELOLRSLTEILKGGVLQIRNPQ
LCYQDTILWKDII FHNKQALTLIDITNRSRACHPCSPMCKGSRWCSSSDCOSLRPT
VCAGCARCKPLPTDCHEQCAAGCTGPKHSDCLACLFHNHSGICELHCPALVTYNT
DTESPMNPSGRVYTFEGASCVTACPNVYLTSDVGSCTLVCPLNHQNQVTAEDGTQCEKC
SKECARQVYGLGHEHLREVAVTSANIQEFAGCKKIFGSLAFIPESDGPASNTAPL
QPEQOVFEILBEITGYLYISAMPDSDUDSVFONQVIRGRIHNGAYSLTLQGLGI
SWGLSRLELGLSLAIHNTLHLCFVHTVPMQLFNPHQALLHTANRPEDECVBEG
LACHQLCARGHGWPGTQCVCNCSQFLRGQECVEECVRLQGLPREYVNAHCLPCHPE
CQPNQSVTCFGEADOCVACAHYKDPFCVAPCPGKPDLSYMPYTWKPFDEBACQ
PCPINCSTCVLDLDDKCPAORASPLTSLISAVVGLLVVVLGVVFGIILKRRQKI
RKYTMRELLQETELVELPTSGAMPNQAOMRILKETBLRKVKVLGSGAFGTVYKGIWI
PDENYKIPVAIKVLRNTSPKANKELDDEAYVWAGVGSYVSRLLGICULTSTVLVT
OLMPYGLLDHVRNRLGSLQDLNMCQIAKMSYLEDVRLVHRDLAARNVGLKSP
NHVKTIDFGLARLLIDIDEYHADGGKVPKMMALLESILRRRFTHQSDVMSYGVYWE
LMTFGAKYPDIPARETPDLLEKGERLPQPICTIDVYIMVMKWMIDSDCRPRFREL
VSFBSMRADPQRFVIONEDLGPASPLDSTFVRSLLDDDDMGDLVDAEYLYVQOQF
CFDPPAPGAGMWHHRSSSTSGSGGDLTLGLEPSEEBAPRPLAPSBGAGSDVDVR
DLGMAKAGLQSLPTHDPSPLQRYSEDTVPLPSETDGYVAPLTCSPQPVYVNPQDVR
PQPSREGELPAAPAGATLERPKTLSPGKNGVVKDVFAGGAVENPEYLTQGGAA
PQPHPPAFSPFDNLYYWDQDPPERGAAPPSTFKGTPTAENPEYLGLDVFPV"

ORIGIN

Alignment Scores:
Pred. No.: 3,85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CQ815384 (1-3768)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCySer 20
Db 946 CCCTGCACCAACCAAGAGGTGACAGCAGAGAGTGAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24

Db 1006 AAGCCCTGTGCC 1017

RESULT 29

CQ841302
LOCUS CQ841302 3768 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 1 from Patent WO2004061105.
ACCESSION CQ841302
VERSION CQ841302.1 GI:50893095
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopitheciidae; Cercopitheciinae; Macaca.

REFERENCE 1
AUTHORS Ciliberto, G.I., Lahm, A.I., la Monica, N.I., Monaci, P.I. and Nuzzo, M.I.
TITLE Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL Patent: WO 2004061105-A 1 22-JUL-2004;
INSTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)

FEATURES

source 1. .3768 Location/Qualifiers
/organism="Macaca mulatta"
/mol_type="unassigned DNA"
/db_xref="taxon:9544"
misc_feature 1. .3768
/note="R = A or G"

ORIGIN

Alignment Scores:
Pred. No.: 3,85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1

Query Match:
DB: 96.97% Indels: 0
Gaps: 0

US-09-632-036F-6 (1-24) x CQ841302 (1-3768)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCySer 20
Db 946 CCCTGCACCAACCAAGAGGTGACAGCAGAGTGAACACACAGCGATGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24

Db 1006 AAGCCCTGTGCC 1017

RESULT 30

CQ841341
LOCUS CQ841341 3768 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 40 from Patent WO2004061105.
ACCESSION CQ841341
VERSION CQ841341.1 GI:50893133
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopitheciidae; Cercopitheciinae; Macaca.

REFERENCE 1

AUTHORS Ciliberto, G.I., Lahm, A.I., la Monica, N.I., Monaci, P.I. and Nuzzo, M.I.
TITLE Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL Patent: WO 2004061105-A 40 22-JUL-2004;
INSTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)

FEATURES

source 1. .3768 Location/Qualifiers
/organism="Macaca mulatta"
/mol_type="unassigned DNA"
/db_xref="taxon:9544"
misc_feature 1. .3768
/note="R = A or G
Y = C or T"

ORIGIN

Alignment Scores:
Pred. No.: 3,85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CQ841341 (1-3768)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCySer 20
Db 946 CCCTGCACCAACCAAGAGGTGACAGCAGAGTGAACACACAGCGATGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24

Db 1006 AAGCCCTGTGCC 1017

RESULT 31

CQ841343
LOCUS CQ841343 3768 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 42 from Patent WO2004061105.
ACCESSION CQ841343
VERSION CQ841343.1 GI:50893134
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopitheciidae; Cercopitheciinae; Macaca.

REFERENCE 1

AUTHORS Ciliberto,G.I., Lahm,A.I., la Monica,N.I., Monaci,P.I. and Nuzzo,M.I.
TITLE Rhesus her2/neu, nucleotides encoding same, and uses thereof
JOURNAL Patent: WO 2004061105-A 42 22-JUL-2004;
ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.
(IT)

FEATURES
source Location/Qualifiers
1..3768
/organism="Macaca mulatta"
/mol_type="unassigned DNA"
/db_xref="taxon:9544"

ORIGIN

Alignment Scores:

Pred. No.: 3.85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CQ841343 (1-3768)

QY 1 ProLeuHisAsnGlnValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 946 CCCTGTCACAAACGAGGTGACAGCGGAGGACGAACACAGCGATGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
|||||

DB 1006 AAGCCTGTGCC 1017

RESULT 32

CQ841344

LOCUS CQ841344 3768 bp DNA linear PAT 02-AUG-2004
DEFINITION Sequence 43 from Patent WO2004061105.
ACCESSION CQ841344
VERSION CQ841344.1 GI:50893135

KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE Macaca mulatta

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Macaca.

1 Ciliberto,G.I., Lahm,A.I., la Monica,N.I., Monaci,P.I. and

Nuzzo,M.I.

Rhesus her2/neu, nucleotides encoding same, and uses thereof

Patent: WO 2004061105-A 43 22-JUL-2004;

ISTITUTO DI RICERCHE DI BIOLOGIA MOLECOLARE P. ANGELETTI S.P.A.

(IT)

FEATURES
source Location/Qualifiers
1..3768
/organism="Macaca mulatta"
/mol_type="unassigned DNA"
/db_xref="taxon:9544"

ORIGIN

Alignment Scores:

Pred. No.: 3.85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CQ841344 (1-3768)

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DB 946 CCCTGTCACAAACGAGGTGACAGCGGAGGACGAACACAGCGATGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
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Db 1006 AAGCCTGTGCC 1017

RESULT 33

CS007994

LOCUS CS007994 3768 bp DNA linear PAT 11-FEB-2005
DEFINITION Sequence 3 from Patent EP1502602.
ACCESSION CS007994

VERSION CS007994.1 GI:59668913

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1

Steinaa,L., Mouritsen,S., Nielsen,K.G., Haaning,J., Leach,D.,

Dalum,I., Gautam,A., Rasmussen,P.B. and Karlsson,G.

Methods for therapeutic vaccination

Patent: EP 1502602-A 3 02-FEB-2005;

Pharmexa A/S (DK)

LOCATION/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 3.85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CS007994 (1-3768)

QY 1 ProLeuHisAsnGlnValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

DB 946 CCCTGTCACAAACGAGGTGACAGAGGTGACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
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DB 1006 AAGCCTGTGCC 1017

RESULT 34

CS020219
LOCUS CS020239 3768 bp DNA linear PAT 23-FEB-2005
DEFINITION Sequence 1 from Patent WO2005012527.
ACCESSION CS020239
VERSION CS020239.1 GI:60220901
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gallo,P.I., Monaci,P.I. and Nuzzo,M.I.
TITLE Synthetic gene encoding human epidermal growth factor 2/neu antigen and uses thereof
JOURNAL Patent: WO 2005012527-A 1 10-FEB-2005;
Istituto di Ricerche di Biologia Molecolare P. Angeletti S.P.A.
(IT)
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source Location/Qualifiers
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Score: 128.00 Matches: 23
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Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
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Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 35
CS104222 3768 bp DNA linear PAT 10-JUN-2005
LOCUS CS104222
DEFINITION Sequence 2 from Patent WO2005049868.
ACCESSION CS104222
VERSION CS104222.1 GI:67512453
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Mehta, A. and Trotta, C.R.
TITLE Methods and agents for screening for compounds capable of modulating her2 expression
JOURNAL Patent: WO 2005049868-A 2 02-JUN-2005;
PCT Therapeutics Inc. (US)
FEATURES
source Location/Qualifiers
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Pred. No.: 3.85e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0

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Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 36
AR409603 3768 bp DNA linear PAT 18-DEC-2003
LOCUS AR409603
DEFINITION Sequence 2 from patent US 6632979.
ACCESSION AR409603
VERSION AR409603.1 GI:40160579
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 3768)
AUTHORS Erickson,S., King,K. and Schwall,R.
TITLE Rodent HER2 tumor model
JOURNAL Patent: US 6632979-A 2 14-OCT-2003;
Genentech, Inc.; South San Francisco, CA
FEATURES
source Location/Qualifiers
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Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
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Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 37
AX060704 3768 bp DNA linear PAT 22-JAN-2001
LOCUS AX060704
DEFINITION Sequence 2 from Patent WO0100244.
ACCESSION AX060704
VERSION AX060704.1 GI:12406101
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Erickson,S. and Schwall,R.
TITLE Methods of treatment using anti-erbB antibody-maytansinoid conjugates
JOURNAL Patent: WO 0100244-A 2 04-JAN-2001;
Genentech, Inc. (US)
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source Location/Qualifiers
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Qy	21 LysProCysAla 24		
Db	1006 AAGCCCTGTGCC 1017		
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DEFINITION	AX201817		
ACCESSION	AX201817		
VERSION	AX201817.1		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
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Cheever, M. A. and Hand-Zimmermann, S.			
Compounds and methods for prevention and treatment of her-2/ neu associated malignancies			
Patent: WO 0153463-A 1 26-JUL-2001;			
CORIXA CORPORATION (US)			
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Query Match:	96.97%	Indels:	0
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US-09-632-036F-6 (1-24) x AX201817 (1-3768)			
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Qy	21 LysProCysAla 24		
Db	1006 AAGCCCTGTGCC 1017		
RESULT 39			
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LOCUS	Sequence 9 from Patent WO0212341.		
DEFINITION	AX380923		
ACCESSION	AX380923		
VERSION	AX380923.1		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
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Cheever, M. A. and Gheysen, D.			
Her-2/neu fusion proteins			
Patent: WO 0212341-A 9 14-FEB-2002;			
CORIXA CORPORATION (US); SMITHKLINE BEECHAM BIOLOGICALS S.A. (BE)			
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Percent Similarity:      95.83%      Conservative:      0
Best Local Similarity:      95.83%      Mismatches:      1
Query Match:      96.97%      Indels:      0
DB:      6      Gaps:      0

US-09-632-036F-6 (1-24) x AX380923 (1-3768)
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ACCESSION      AX384604
VERSION      AX384604.1 GI:19577806
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Hand-Zimmermann,S., Cheever,M.A., Foy,T.M., Lodes,M.J., Kalos,M.D.,
McNeill,P.D. and Vedvick,T.S.
TITLE      Compositions and methods for the therapy and diagnosis of
her-2/neu-associated malignancies
JOURNAL      Patent: WO 0214503-A.1 21-FEB-2002;
CORIXA CORPORATION (US)
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ORIGIN
Alignment Scores:
Pred. No.:      3.85e-10      Length:      3768
Score:      128.00      Matches:      23
Percent Similarity:      95.83%      Conservative:      0
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US-09-632-036F-6 (1-24) x AX384604 (1-3768)
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Perfect score: 132

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Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	128	97.0	471	6	ABK29542 Colon ade
2	128	97.0	670	10	ACD96468 Human col
3	128	97.0	1219	14	ADZ69875 p185neu o
4	128	97.0	1255	11	ADM29353 Human nov

5	128	97.0	1260	10	ADF16383
6	128	97.0	1320	14	ADZ47818
7	128	97.0	1459	14	ADZ69874
8	128	97.0	1555	8	ACC83226
9	128	97.0	1699	14	ADZ69873
10	128	97.0	1872	2	AAQ06828
11	128	97.0	1939	14	ADZ69872
12	128	97.0	1944	14	ADZ47796
13	128	97.0	1956	12	ADJ57171
14	128	97.0	2028	14	ADM87396
15	128	97.0	2028	14	ADM87397
16	128	97.0	2052	12	ADJ57170
17	128	97.0	2061	14	ADZ47808
18	128	97.0	2086	14	ADZ69880
19	128	97.0	2086	14	ADZ69879
20	128	97.0	2086	14	ADZ69881
21	128	97.0	2086	14	ADZ69882
22	128	97.0	2132	10	ADG17937
23	128	97.0	2149	10	ADG17943
24	128	97.0	2164	10	ADG17939
25	128	97.0	2261	11	ADM29355
26	128	97.0	2320	14	ADZ47794
27	128	97.0	2385	2	AAT72725
28	128	97.0	2437	14	ADZ47806
29	128	97.0	2802	13	ADT50728
30	128	97.0	2871	3	AAZ50586
31	128	97.0	3188	11	ADM29351
32	128	97.0	3600	3	AAA89736
33	128	97.0	3678	6	ABK86207
34	128	97.0	3765	10	ADB67620
35	128	97.0	3765	14	ADZ72379
36	128	97.0	3768	2	AAT40739
37	128	97.0	3768	2	AAT40739
38	128	97.0	3768	3	AAA09455
39	128	97.0	3768	5	AAH23392
40	128	97.0	3768	6	ABV78168
41	128	97.0	3768	6	ABZ35744
42	128	97.0	3768	6	AAD32743
43	128	97.0	3768	6	ABK10730
44	128	97.0	3768	6	AAD43935
45	128	97.0	3768	6	ABX09987
46	128	97.0	3768	6	AAD43986
47	128	97.0	3768	6	ABK14058
48	128	97.0	3768	6	ABA92250
49	128	97.0	3768	6	ABU91709
50	128	97.0	3768	8	ACC57649
51	128	97.0	3768	13	ADQ75970
52	128	97.0	3768	13	ADQ75929
53	128	97.0	3768	13	ADQ75968
54	128	97.0	3768	13	ADQ75971
55	128	97.0	3768	14	ADV43219
56	128	97.0	3768	14	ADM87389
57	128	97.0	3768	14	AEA47578
58	128	97.0	3778	14	ADM87398
59	128	97.0	4299	2	AAQ46083
60	128	97.0	4472	3	AAA14812
61	128	97.0	4473	2	ABQ76220
62	128	97.0	4473	2	AAZ31071
63	128	97.0	4473	6	ABZ34969
64	128	97.0	4473	6	ABZ38904
65	128	97.0	4473	8	ACC69999
66	128	97.0	4473	10	ADC35148
67	128	97.0	4473	10	ADD25483
68	128	97.0	4473	12	ADQ17192
69	128	97.0	4478	12	ADQ83974
70	128	97.0	4529	12	ADJ57169
71	128	97.0	4530	2	AAT01585
72	128	97.0	4530	2	AAT71253
73	128	97.0	4530	3	AAZ60815
74	128	97.0	4530	4	ABN19731
75	128	97.0	4530	6	ABN85585
76	128	97.0	4530	6	ABZ35012
77	128	97.0	4530	6	ABV94128

Adf16383	Human alb
Adz47818	DNA encod
Adz69874	p185neu o
Acc83226	Expressio
Adz69873	p185neu o
Aaq06828	Extracell
Adz69872	p185neu o
Adz47796	DNA encod
Adj57171	Her-2/neu
Adw87396	Human cod
Adw87397	Human wil
Adj57170	Human Her
Adz47808	DNA encod
Adz69880	p185neu o
Adz69879	p185neu o
Adz69881	p185neu o
Adz69882	p185neu o
Adg17937	Human HER
Adg17943	Human HER
Adg17939	Human HER
Adm29355	Human nov
Adz47794	DNA encod
Aat72725	Her2-GM-C
Adz47806	DNA encod
Adt50728	Cancer re
Aaz50586	DC8cFv-e
Adm29351	Human nov
Aaa89736	Human HER
Abk86207	CDNA enco
Adb67620	Human epi
Adz72379	DNA encod
Aat40739	HER-2/neu
Aax01912	Human HER
Aaa09455	Human her
Aah23392	Human HER
Abv78168	Human ERB
Abz35744	Human ERB
Aad32743	Human Her
Abk10730	Human Her
Aad43935	Human HER
Abx09987	Human ERB
Aad43986	Human ERB
Abk14058	Human HER
Abag2250	Human Her
Abu91709	Human pol
Acc57649	Human pro
Adq75970	Rhesus mo
Adq75929	Rhesus mo
Adq75968	Rhesus mo
Adq75971	Rhesus mo
Adv43219	Human pay
Adw87389	Human cod
Aea47578	Nucleotid
Adw87398	Human cod
Aaq46083	Sequence
Aaa14812	cdNA enco
Abq76220	Human tum
Aaz31071	HER-2 nuc
Abz34969	Human gen
Abz38904	Human Her
Acc69999	Human c-e
Adc35148	Human bre
Add25483	Binding d
Adq17192	Human sof
Adg83974	Human tum
Adj57169	Human Her
Aat01585	Her-2/neu
Aat71253	Human HER
Aaz60815	Nucleotid
Abn19731	Human tyr
Abn85585	Human HER
Abz35012	Human gen
Abv94128	Breast ca

```

78 128 97.0 4530 6 ABK83918
79 128 97.0 4530 8 ACC50139
80 128 97.0 4530 8 ABQ83856
81 128 97.0 4530 9 AAD58073
82 128 97.0 4530 10 ADC09594
83 128 97.0 4530 12 ADH13161
84 128 97.0 4530 12 ADJ32564
85 128 97.0 4530 12 ADM72832
86 128 97.0 4530 12 ADO20008
87 128 97.0 4530 12 ADG29633
88 128 97.0 4530 13 ACN40176
89 128 97.0 4530 13 ADR83426
90 128 97.0 4530 14 ADW44364
91 128 97.0 4530 14 ADW28639
92 128 97.0 4530 14 ADY61191
93 128 97.0 4530 14 ADZ09642
94 128 97.0 4530 14 AEA15048
95 128 97.0 4530 14 AEA08354
96 128 97.0 4559 13 ADT50724
97 128 97.0 4606 10 ADB47370
98 128 97.0 4642 11 ACN89746
99 128 97.0 4647 14 ADZ47802
100 128 97.0 4806 14 ADY30408

```

ALIGNMENTS

```

RESULT 1
ABK29542
ID ABK29542 standard; cDNA; 471 BP.
XX
AC ABK29542;
XX
DT 23-APR-2002 (first entry)
XX
DE Colon adenocarcinoma-specific cDNA #68.
XX
KW Human; colon adenocarcinoma; colon cancer; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200196389-A2.
XX
PD 20-DEC-2001.
XX
PF 07-JUN-2001; 2001WO-US018574.
XX
PR 09-JUN-2000; 2000US-0210667P.
PR 22-NOV-2000; 2000US-0252614P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Meagher MJ, King GE, Xu J, Secrist H;
XX
WPI; 2002-098052/13.
XX
PT New isolated polynucleotide encoding a polypeptide comprising a portion
PT of colon tumor protein, for detection, diagnosis and therapy of human
PT colon cancer.
XX
PS Claim 1; Page 133; 21lpp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding a
CC polypeptide (II) comprising a portion of a colon tumour protein. A new
CC oligonucleotide (III) that hybridises to (I) is useful for determining
CC the presence of a cancer in a patient. (II) or antigen presenting cells
CC expressing (I) are useful for stimulating and/or expanding T cells
CC specific for a tumour protein, by contacting T cells with (I), (II) or
CC antigen-presenting cells that express (I), (II), or antigen
CC presenting cells that express (II) are useful for treating colon cancer
CC in a patient by incubating CD4+ and/or CD8+ T cells isolated from a
CC patient with (I), (II), or antigen presenting cells that express (II), so
CC that T cells proliferate, and administering to the patient an effective

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CC amount of the proliferated T cells, thus inhibiting the development of a
CC cancer in the patient. A new composition is useful for stimulating an
CC immune response in a patient. (I) or (II) is useful in vaccines and
CC pharmaceutical compositions for prevention and treatment of colon cancer
CC and for the diagnosis and monitoring of the cancers. (I), (II) or an
CC antibody against (II) is useful for detection, diagnosis and/or therapy
CC of human colon cancer. (I) is useful as a probe or primer for nucleic
CC acid hybridisation, and in the design and preparation of ribozyme
CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
CC ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of
CC the invention

```

SQ Sequence 471 BP; 104 A; 136 C; 135 G; 96 T; 0 U; 0 Other;

```

Alignment Scores:
Pred. No.: 3,36e-11 Length: 471
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

```

US-09-632-036F-6 (1-24) x ABK29542 (1-471)

```

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 65 CCCCTGTCACCAAGAGGTGACAGAGAGTGAACACACACGCGGTGTGAGAAAGTCAGC 124
QY 21 LysProCysAla 24
Db 125 AAGCCCTGTGCC 136

```

RESULT 2

ACD96468/c
ID ACD96468 standard; cDNA; 670 BP.

XX ACD96468;

XX 23-SEP-2003 (first entry)

XX Human colon cancer cell expressed cDNA #4880.

Open reading frame detection; genome sequencing; colon cancer;
breast cancer; population genome analysis; genetic shift; cancer;
antibiotic resistance; antibiotic non-tolerance; congenital disease;
agriculture; food crop genome; resistance gene; retrovirus;
influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
gene; ss.

XX Homo sapiens.

XX US2002155438-A1.

XX 24-OCT-2002.

XX 27-SEP-1999; 99US-00406117.

XX 20-NOV-1998; 98US-00196716.

(SIMP/) SIMPSON A J G.

(NETO/) NETO E D.

(BRENT/) BRENTANI R R.

XX Simpson AJG, Neto ED, Brentani RR;

XX WPI; 2003-182626/18.

Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.

XX Example 9; Page 701; 959pp; English.

XX The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence of a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX

SQ Sequence 670 BP; 133 A; 187 C; 206 G; 142 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 5.18e-11 Length: 670
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 10 Gaps: 0

US-09-632-036F-6 (1-24) x ACD96468 (1-670)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 157 CCCTGCACCAACCAAGAGGTGACAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 98

Qy 21 LysProCysAla 24
Db 97 AAGCCCTGTGCC 86

RESULT 3

ID ADM269875
ADZ69875 standard; cDNA; 1219 BP.

XX ADM269875;

DT 14-JUL-2005 (first entry)

DE p185neu oncoprotein-encoding cDNA, SEQ ID 6.

KW gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;
KW vaccine; ss; pharmaceutical.

OS Homo sapiens.

OS Rattus sp.

OS Chimeric.

XX WO2005039618-A1.

XX 06-MAY-2005.
PD
XX
XX
PF 06-OCT-2004; 2004WO-EP011161.
XX
PR 09-OCT-2003; 2003IT-MI001942.
XX
XX (INDE-) INDENA SPA.
XX
XX Amici A, Cavallo F, Fornì G, Marchini C;
PI
XX
XX WPI; 2005-322913/33.
DR

XX New DNA transfer vector containing a sequence coding for a p185neu-
PT fragment, useful for preparing a pharmaceutical composition for treating
PT tumors, and for preparing DNA vaccine.
XX

PS Claim 1; SEQ ID NO 6; 64pp; English.

XX The invention relates to a DNA transfer vector containing a sequence
CC coding for a p185neu-fragment. Also described are: a pharmaceutical
CC composition comprising the DNA vector in admixture with vehicles and
CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further
CC contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapses of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.

XX SQ Sequence 1219 BP; 228 A; 380 C; 375 G; 236 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.08e-10 Length: 1219
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69875 (1-1219)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 110 CCCTGCACCAACCAAGAGGTGACAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 169

Qy 21 LysProCysAla 24
Db 170 AAGCCCTGTGCC 181

RESULT 4

ID ADM29353
ADM29353 standard; DNA; 1255 BP.

XX ADM29353;

XX 20-MAY-2004 (first entry)

DT Human novel protein NOV20b coding sequence.

DE human; novel protein; NOV; cancer; immune associated disorder; gene; ds.

KW Homo sapiens.

OS WO2003064628-A2.

XX

XX 07-AUG-2003.

XX

XX 03-FEB-2003; 2003WO-US003401.

XX

XX 01-FEB-2002; 2002US-0353287P.

```
PR 01-FEB-2002; 2002US-0353301P.
PR 12-FEB-2002; 2002US-0356371P.
PR 13-FEB-2002; 2002US-0356424P.
PR 13-FEB-2002; 2002US-0356531P.
PR 20-FEB-2002; 2002US-0358239P.
PR 26-FEB-2002; 2002US-0359603P.
PR 27-FEB-2002; 2002US-0359848P.
PR 27-FEB-2002; 2002US-0359860P.
PR 15-MAR-2002; 2002US-0365049P.
PR 22-MAR-2002; 2002US-0366802P.
PR 17-MAY-2002; 2002US-0381666P.
PR 18-JUN-2002; 2002US-0389531P.
PR 19-JUN-2002; 2002US-0389910P.
PR 25-JUN-2002; 2002US-0391516P.
PR 02-JUL-2002; 2002US-0393265P.
PR 07-AUG-2002; 2002US-0401825P.
PR 09-AUG-2002; 2002US-0402395P.
PR 12-AUG-2002; 2002US-0402867P.
PR 23-AUG-2002; 2002US-0405401P.
PR 23-AUG-2002; 2002US-0405820P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Alsobrook JP, Bader JS, Berghs C, Burgess CE, Casman SJ;
PI Catterton E, Chaudhuri A, Edinger SR, Ellerman K, Gerlach VL;
PI Gorman L, Guo X, Herrmann JL, Ji W, Khrantsov NV, Li L, Miller CE;
PI Ort T, Patturajan M, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
PI Spytek KA, Vernet CAM, Zhong H, Zhong M;
XX
XX WPI; 2003-646149/61.
DR P-PSDB; ADM29354.
XX
XX New NOVX polypeptide, useful for the manufacture of a medicament for
PT treating e.g., cancer or immune associated disorders.
XX
XX Claim 20; SEQ ID NO 97; 606pp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel
CC human proteins (NOV proteins). The DNA and protein sequences of the
CC invention are useful for the manufacture of a medicament for treating a
CC syndrome associated with a human disease comprising a pathology
CC associated with the protein, such as: cancer or immune associated
CC disorders. The present DNA sequence encodes a NOV protein of the
CC invention.
XX
XX Sequence 1255 BP; 256 A; 415 C; 360 G; 224 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.12e-10 Length: 1255
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 11 Gaps: 0
US-09-632-036f-6 (1-24) x ADM29353 (1-1255)
Qy 1 ProteuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 971 CCCCTGCACCAACCAAGGTTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGACG 1030
Qy 21 LysProCysAla 24
Db 1031 AAGCCCTGTGCC 1042
RESULT 5
ADFI6383
ID ADFI6383 standard; DNA; 1260 BP.
XX
XX ADFI6383;
XX
XX 12-FEB-2004 (first entry)
XX
```

```
DE Human albumin fusion protein-related DNA sequence SeqID1475.
XX
XX albumin fusion protein; albumin activity; human serum albumin;
KW serum osmotic pressure; shelf-life; stability; antidiabetic;
KW gene therapy; diabetes mellitus; human; gene; ds.
XX
XX Homo sapiens.
XX
XX WO2003060071-A2.
XX
XX 24-JUL-2003.
XX
XX 23-DEC-2002; 2002WO-US040891.
XX
XX 21-DEC-2001; 2001US-0341811P.
PR 24-JAN-2002; 2002US-0350358P.
PR 28-JAN-2002; 2002US-0351360P.
PR 26-FEB-2002; 2002US-0359370P.
PR 28-FEB-2002; 2002US-0360000P.
PR 27-MAR-2002; 2002US-0367500P.
PR 08-APR-2002; 2002US-0370227P.
PR 10-MAY-2002; 2002US-0378950P.
PR 24-MAY-2002; 2002US-0382617P.
PR 28-MAY-2002; 2002US-0383123P.
PR 05-JUN-2002; 2002US-0385708P.
PR 10-JUL-2002; 2002US-0394625P.
PR 24-JUL-2002; 2002US-0398008P.
PR 09-AUG-2002; 2002US-0402131P.
PR 13-AUG-2002; 2002US-0402708P.
PR 18-SEP-2002; 2002US-0411355P.
PR 18-SEP-2002; 2002US-0411426P.
PR 02-OCT-2002; 2002US-0414984P.
PR 11-OCT-2002; 2002US-0417611P.
PR 23-OCT-2002; 2002US-0420246P.
PR 05-NOV-2002; 2002US-0423623P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (DELZ) DELTA BIOTECHNOLOGY LTD.
PA (PRIN-) PRINCIPIA PHARM CORP.
XX
XX Ballance DJ, Turner AJ, Rosen CA, Haseltine WA;
PI WPI; 2003-598517/56.
XX P-PSDB; ADF16709.
XX
XX New albumin fusion protein, useful for preparing a composition for
PT treating diabetes mellitus.
XX
XX Example 4; SEQ ID NO 1475; 24pp; English.
XX
XX This invention relates to a novel albumin fusion protein having albumin
CC or biological activity. Human serum albumin is responsible for a
CC significant proportion of the osmotic pressure of serum and also
CC functions as a carrier of endogenous and exogenous ligands. The fusion of
CC albumin to a therapeutic protein may increase shelf-life and stability of
CC the therapeutic protein. The albumin fusion protein of the invention may
CC allow production of compositions with antidiabetic activity whilst the
CC nucleotide sequence which encodes it may be useful for gene therapy. The
CC albumin fusion protein which encodes it is useful for preparing a composition for treating
CC diabetes mellitus. The present sequence is a DNA sequence which encodes a
CC therapeutic protein which was fused with human albumin to create a novel
CC albumin fusion protein of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/publishedpct_sequences
XX
XX Sequence 1260 BP; 238 A; 441 C; 340 G; 241 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1.13e-10 Length: 1260
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
```

Query Match: 96.97% Indels: 0
DB: 10 Gaps: 0

US-09-632-036F-6 (1-24) x ADF16383 (1-1260)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 6
ADZ47818
ID ADZ47818 standard; DNA; 1320 BP.
AC ADZ47818;
XX 30-JUN-2005 (first entry)
XX DNA encoding human ErbB-2 variant VI.
XX epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic; gene; ds.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 151..1314
FT /tag= a
FT /product= "ErbB-2 variant VI"
FT CDS 1171..1314
FT /tag= b
FT /product= "Active region of ErbB-2 variant VI"
FT /note= "Given as SEQ ID No:27, specifically claimed in
Claim 170"
XX
XX WO200503133-A2.
XX
XX 14-APR-2005.
XX
XX 04-OCT-2004; 2004WO-US030903.
XX
XX 03-OCT-2003; 2003US-0507953P.
XX 10-NOV-2003; 2003US-0518321P.
XX 09-AUG-2004; 2004US-0599583P.
XX 07-SEP-2004; 2004US-0607326P.
XX
XX (COMP-) COMPUTEN LTD.
XX (COMP-) COMPUTEN INC.
XX
XX Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
XX Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX
XX WPI: 2005-285403/29.
XX P-PSDB; ADZ47818.
XX
XX New isolated polynucleotide encoding at least an active portion of an
XX ErbB-2 polypeptide, useful for diagnosing or treating diseases with
XX aberrant expression or activity of the ErbB-2 polypeptides, such as
XX cancer.
XX
XX Claim 70; SEQ ID NO 25; 246pp; English.
XX
XX The invention relates to the isolation of polynucleotide sequences
XX encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
XX HER-2 or neu) polypeptides. Also described are methods, compositions, and
XX kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
XX treatment of ErbB-2 related cancer. The sequences, methods, and
XX compositions of the present invention are useful for diagnosing,
XX prognosing, and/or treating diseases or conditions associated with
XX aberrant expression or activity of the ErbB-2 polypeptides, such as

CC cancer. This sequence encodes human ErbB-2 variant VI.
XX
SQ Sequence 1320 BP; 261 A; 462 C; 371 G; 226 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.19e-10 Length: 1320
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ47818 (1-1320)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 7
ADZ69874
ID ADZ69874 standard; cDNA; 1459 BP.
XX AC ADZ69874;
XX
XX 14-JUL-2005 (first entry)
XX
XX p185neu oncoprotein-encoding cDNA, SEQ ID 5.
XX gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;
XX vaccine; ss; pharmaceutical.
XX Homo sapiens.
XX Rattus sp.
XX Chimeric.
XX
XX WO2005039618-A1.
XX
XX 06-MAY-2005.
XX
XX 06-OCT-2004; 2004WO-EP011161.
XX
XX 09-OCT-2003; 2003IT-MI001942.
XX
XX (INDE-) INDENA SPA.
XX
XX Amici A, Cavallo F, Forni G, Marchini C;
XX
XX WPI: 2005-322913/33.
XX
XX New DNA transfer vector containing a sequence coding for a p185neu-
XX fragment, useful for preparing a pharmaceutical composition for treating
XX tumors, and for preparing DNA vaccine.
XX
XX Claim 1; SEQ ID NO 5; 64pp; English.
XX
XX The invention relates to a DNA transfer vector containing a sequence
XX coding for a p185neu-fragment. Also described are: a pharmaceutical
XX composition comprising the DNA vector in admixture with vehicles and
XX excipient; and a combined pharmaceutical preparation containing at least
XX two different plasmids for simultaneous, sequential or separate
XX therapeutic use. The DNA transfer vector is a plasmid, which further
XX contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid
XX is useful in the therapeutic treatment of subjects at risk of developing
XX p185neu positive tumors, or of patients having primary tumors, metastasis
XX or relapses of p185neu-expressing tumors. The plasmid is also useful for
XX the preparation of DNA vaccine. The present sequence represents a p185neu
XX -encoding fragment used in the plasmids of the invention.
XX
XX Sequence 1459 BP; 272 A; 467 C; 434 G; 286 T; 0 U; 0 Other;
SQ

```
Alignment Scores:
Pred. No.: 1.35e-10 Length: 1459
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US 09-632-036F-6 (1-24) x ADZ69874 (1-1459)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
   |||||||
Db 350 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 409
   |||||||

QY 21 LysProCysAla 24
   |||||||
Db 410 AAGCCCTGTGCC 421

RESULT 8
ACC83226
ID ACC83226 standard; DNA; 1555 BP.
XX
AC ACC83226;
XX
XX 05-SEP-2003 (first entry)
XX
DE Expression vector pCDNA3-hSIDDD DNA.
XX
KW DNA tumour; vaccine; pCDNA3-hSIDDD; vector; ds.
XX
OS Unidentified.
XX
PN CN1380107-A.
XX
PD 20-NOV-2002.
XX
PF 27-SEP-2001; 2001CN-00126890.
XX
XX 27-SEP-2001; 2001CN-00126890.
XX
XX (UYFU-) UNIV FUDAN.
XX
PI He Q, Wang Y, Zhang Y;
XX
DR WPI; 2003-222532/22.
XX
PT DNA tumor vaccine and its preparation method.
XX
PS Claim 1; Page 8; 20pp; Chinese.
XX
CC The invention relates to a novel DNA tumour vaccine. Also disclosed is a
CC method for preparing the vaccine comprising, adopting a specific fragment
CC hSIDDD of clonal human HER-2/neu and utilising NotI/XhoI double enzyme
CC sections to directionally insert them into the pcDNA3 plasmid to
CC construct the human HER-2/neu gene eucaryon expression vector pCDNA3-
CC hSIDDD. The current sequence represents the expression vector pCDNA3-hSIDDD
CC DNA
XX
SQ Sequence 1555 BP; 306 A; 527 C; 444 G; 278 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.46e-10 Length: 1555
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 8 Gaps: 0

US-09-632-036F-6 (1-24) x ACC83226 (1-1555)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
   |||||||
```

```
Db 1091 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1150
QY 21 LysProCysAla 24
   |||||||
Db 1151 AAGCCCTGTGCC 1162

RESULT 9
ADZ69873
ID ADZ69873 standard; cDNA; 1699 BP.
XX
AC ADZ69873;
XX
XX 14-JUL-2005 (first entry)
XX
DE p185neu oncoprotein-encoding cDNA, SEQ ID 4.
XX
KW gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;
KW vaccine; ss; pharmaceutical.
XX
OS Homo sapiens.
OS Rattus sp.
OS Chimeric.
PN WO2005039618-A1.
XX
XX 06-MAY-2005.
XX
XX 06-OCT-2004; 2004WO-EP011161.
XX
XX 09-OCT-2003; 2003IT-MI001942.
XX
XX (INDE-) INDENA SPA.
XX
XX Amici A, Cavallo F, Forni G, Marchini C;
XX
XX WPI; 2005-322913/33.
XX
PT New DNA transfer vector containing a sequence coding for a p185neu-
PT fragment, useful for preparing a pharmaceutical composition for treating
PT tumors, and for preparing DNA vaccine.
XX
XX Claim 1; SEQ ID NO 4; 64pp; English.
XX
CC The invention relates to a DNA transfer vector containing a sequence
CC coding for a p185neu-fragment. Also described are: a pharmaceutical
CC composition comprising the DNA vector in admixture with vehicles and
CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further
CC contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapses of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.
XX
XX Sequence 1699 BP; 319 A; 541 C; 505 G; 334 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.62e-10 Length: 1699
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69873 (1-1699)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
   |||||||
Db 590 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 649
   |||||||
QY 21 LysProCysAla 24
```

XX	HER2 extracellular domain used as vaccine - comprises sequence of at least 9 aminoacid(s) prep'd. using expression vector of DNA isolated from human epidermal growth factor receptor.	XX	Alignment Scores:
PT		XX	Pred. No.:
PT		XX	Score:
PT		XX	Best Local Similarity:
PS	Disclosure; Fig 13; 49pp; English.	XX	Best Local Similarity:
XX		XX	Query Match:
XX		XX	DB:
CC	This claimed sequence terminates 1 bp, pref. 24 bps, upstream of the DNA portion encoding the transmembrane domain of the HER2 mol. It encodes none of the transmembrane or intracellular portions of the HER2 mol. The protein is antigenic in animals. The sequence can be used to produce an extracellular portion of the HER2 mol. comprising at least 9 amino acids. The product opens several possibilities for further research and a broad range of potential therapeutic applications, eg. for the treatment of CC mammary gland adenocarcinoma and other cancers	XX	US-09-632-036F-6 (1-24) x AAQ06828 (1-1872)
XX		XX	Qy
XX		XX	Dy
XX		XX	Qy
XX		XX	Dy
XX		XX	RESULT 11
XX		XX	ADZ69872
XX		XX	ID
XX		XX	AC
XX		XX	XX
XX		XX	DT
XX		XX	XX
XX		XX	DE
XX		XX	XX
XX		XX	KW
XX		XX	OS
XX		XX	OS
XX		XX	XX
XX		XX	PN
XX		XX	XX
XX		XX	PD
XX		XX	PF
XX		XX	PR
XX		XX	XX
XX		XX	PA
XX		XX	PI
XX		XX	XX
XX		XX	DR
XX		XX	XX
XX		XX	PT
XX		XX	PT
XX		XX	XX
XX		XX	PS
XX		XX	XX

CC The invention relates to a DNA transfer vector containing a sequence
CC coding for a p185neu-fragment. Also described are: a pharmaceutical
CC composition comprising the DNA vector in admixture with vehicles and
CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further
CC contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapses of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.
XX
SQ Sequence 1939 BP; 373 A; 615 C; 574 G; 377 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.91e-10 Length: 1939
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69872 (1-1939)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 830 CCCTGTCACACCAACGAGGTGACAGCAGAGGATGGAAACACACGCGGTGTGAGAAGTGCAGC 889
|||
QY 21 LysProCysAla 24
|||
Db 890 AAGCCCTGTGCC 901
|||

RESULT 12

ADZ47796
ID ADZ47796 standard; DNA; 1944 BP.

XX AC ADZ47796;

XX DT 30-JUN-2005 (first entry)

XX DE DNA encoding human ErbB-2 variant II.

XX epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic; gene; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 151..1878

FT FT /*tag= a

FT FT /product= "ErbB-2 variant II"

FT FT 1664..1944

FT FT /*tag= b

FT FT /product= "Active region of ErbB-2 variant II"

FT FT /note= "Given as SEQ ID No:8, specifically claimed in

FT FT Claim 10"

XX WO2005033133-A2.

XX PN

XX PD 14-APR-2005.

XX PF 04-OCT-2004; 2004WO-US030903.

XX PR 03-OCT-2003; 2003US-0507953P.

XX PR 10-NOV-2003; 2003US-0518321P.

XX PR 09-AUG-2004; 2004US-0599583P.

XX PR 07-SEP-2004; 2004US-0607326P.

XX (COMP-) COMPUGEN LTD.

XX (COMP-) COMPUGEN INC.

XX Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;

PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX
DR WPI: 2005-285403/29.
P-PSDB; ADZ47797.
XX
PT New isolated polynucleotide encoding at least an active portion of an
PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
PT aberrant expression or activity of the ErbB-2 polypeptides, such as
PT cancer.

XX Claim 8; SEQ ID NO 3; 246pp; English.

XX The invention relates to the isolation of polynucleotide sequences
CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
CC treatment of ErbB-2 related cancer. The sequences, methods, and
CC compositions of the present invention are useful for diagnosing,
CC prognosing, and/or treating diseases or conditions associated with
CC aberrant expression or activity of the ErbB-2 polypeptides, such as
CC cancer. This sequence encodes human ErbB-2 variant II.

SQ Sequence 1944 BP; 370 A; 671 C; 539 G; 364 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.92e-10 Length: 1944
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ47796 (1-1944)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 1096 CCCTGTCACACCAACGAGGTGACAGCAGAGGATGGAAACACACGCGGTGTGAGAAGTGCAGC 1155
|||

QY 21 LysProCysAla 24
|||

Db 1156 AAGCCCTGTGCC 1167
|||

RESULT 13

ADJ57171

ID ADJ57171 standard; cDNA; 1956 BP.

XX AC ADJ57171;

XX DT 06-MAY-2004 (first entry)

XX DE Her-2/neu gene lacking intracellular region and transmembrane domain.

XX KW Her-2/neu; vaccine; cancer; glycoprotein D; cytostatic; human;
KW gene; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX WO2004007734-A1.

XX PN

XX PD 22-JAN-2004.

XX PF 15-JUL-2003; 2003WO-KR001400.

XX PR 16-JUL-2002; 2002KR-00041764.

XX PR 12-JUN-2003; 2003KR-00038012.

XX (PANG-) PANGENOMICS CO LTD.

XX Lee JY, Kim D, Chung Y, Chang S, Lee K, Kang C;

XX WPI: 2004-122962/12.

XX

PT New Her-2/neu plasmid construct having anti-cancer activity, useful for
PT preparing a DNA vaccine for preventing and/or treating cancer.
XX
PS Claim 5; SEQ ID NO 3; 70pp; English.
XX
CC The invention relates to an Her-2/neu plasmid construct having anti-
CC cancer activity that is prepared by inserting a truncated human Her-2/neu
CC gene lacking the intracellular domain into plasmid pTV2 or pCK. Aslo
CC provided are a DNA vaccine for preventing and/or treating cancer
CC comprising the plasmid construct and a carrier; and a method for
CC preventing and/or treating cancer by administering the DNA vaccine cited
CC above. The construct is pHER2 (KCCM-10393), pCKTM (KCCM-10396), pNeuECD
CC (KCCM-10394) or pCKECD (KCCM-10395). The truncated human Her-2/neu gene
CC further lacks the transmembrane domain. The signal peptide of the human
CC Her-2/neu gene is replaced by the signal peptide of herpes simplex type 1
CC glycoprotein D (gD). The plasmid construct is preferably pNeuTM-gs. The
CC plasmid construct further translates a cytokine gene besides the human
CC Her-2/neu gene. The cytokine gene is selected from granulocyte-macrophage
CC colony-stimulating factor (GM-CSF), FMS-like tyrosine kinase 3 ligand
CC (Flt3L), early T lymphocyte activation-1 (Eta-1), interleukin-12 (IL-12),
CC IL-15 and IL-18. The DNA vaccine further comprises a cytokine gene
CC expressing plasmid. The Her-2/neu plasmid construct is useful for
CC preparing a DNA vaccine for treating and/or preventing cancer. The
CC present sequence represents the nucleotide sequence of the human Her-
CC 2/neu gene lacking the intracellular region and transmembrane domain.
XX
SQ Sequence 1956 BP; 383 A; 640 C; 567 G; 366 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.93e-10 Length: 1956
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 12 Gaps: 0

US-09-632-036F-6 (1-24) x ADJ5171 (1-1956)

OY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCACACCCAGAGGTGACACGACAGAGATGGAAACACAGCGGTGTGAGAAAGTGCAGC 1005
OY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 14

ID ADW87396 standard; DNA; 2028 BP.

AC ADW87396;

DT 21-APR-2005 (first entry)

DE Human codon-optimized HER2ECDTM DNA.

KW human epidermal growth factor 2; HER2ECDTM; cancer; neoplasm; Cytostatic;
KW vaccine; ds; gene.

OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..2028

FT /*tag= a

FT /product= "HER2ECDTM"

XX WO2005012527-A1.

PN 10-FEB-2005.

XX 20-JUL-2004; 2004WO-EP008234.

XX 21-JUL-2003; 2003US-0489237P.

XX

XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

XX Gallo P, Monaci P, Nuzzo M;

XX WPI; 2005-123289/13.

XX P-PSDB; ADW87401.

XX New synthetic nucleic acid molecule encoding human epidermal growth
PT factor 2 (HER2)/neu or HER2ECDTM protein, useful for preventing or
PT treating HER2-associated cancer.

XX Claim 7; SEQ ID NO 9; 62pp; English.

XX The invention relates to a synthetic nucleic acid molecule which
CC comprises a sequence of nucleotides: (a) encoding a human epidermal
CC growth factor 2 (HER2)/neu protein; (b) encoding a human HER2ECDTM
CC protein; and (c) encoding a variant human HER2/neu or HER2ECDTM
CC polypeptide. The sequences, vector, vaccine, composition, and methods are
CC useful for preventing or treating HER2-associated cancer. The present
CC sequence represents the human codon-optimized HER2ECDTM DNA.

XX SQ Sequence 2028 BP; 338 A; 802 C; 619 G; 269 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.02e-10 Length: 2028
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADW87396 (1-2028)

OY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCACACCCAGAGGTGACCCGCGAGGACCGCACCCAGCGCTCGGAGAAAGTGCAGC 1005

OY 21 LysProCysAla 24

Db 1006 AAGCCCTGTGCC 1017

RESULT 15

ID ADW87397

XX ADW87397 standard; DNA; 2028 BP.

AC ADW87397;

XX 21-APR-2005 (first entry)

XX Human wild type HER2ECDTM DNA.

XX human epidermal growth factor 2; HER2ECDTM; cancer; neoplasm; Cytostatic;
KW vaccine; ds; gene.

OS Homo sapiens.

XX WO2005012527-A1.

PN 10-FEB-2005.

XX 20-JUL-2004; 2004WO-EP008234.

XX 21-JUL-2003; 2003US-0489237P.

XX

XX (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.

XX Gallo P, Monaci P, Nuzzo M;

XX WPI; 2005-123289/13.

XX New synthetic nucleic acid molecule encoding human epidermal growth
PT factor 2 (HER2)/neu or HER2ECDTM protein, useful for preventing or
PT

PT treating HER2-associated cancer.
XX Disclosure; SEQ ID NO 10; 62pp; English.
PS
XX The invention relates to a synthetic nucleic acid molecule which
CC comprises a sequence of nucleotides: (a) encoding a human epidermal
CC growth factor 2 (HER2)/neu protein; (b) encoding a human HER2ECDTM
CC polypeptide. The sequences, vector, vaccine, composition, and methods are
CC useful for preventing or treating HER2-associated cancer. The present
CC sequence represents the human wild-type HER2ECDTM DNA.
XX
SQ Sequence 2028 BP; 389 A; 656 C; 591 G; 392 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,02e-10 Length: 2028
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADW87397 (1-2028)

QY 1 ProLeuHisAsnGlnValThrAlaGluAspGlyThrGlnArgAlaGluIysCysSer 20
DB 946 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCACG 1005
QY 21 LysProCysAla 24
DB 1006 AAGCCCTGTGCC 1017

RESULT 16
ADJ57170
ID ADJ57170 standard; cDNA; 2052 BP.
XX
AC ADJ57170;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human Her-2/neu gene lacking intracellular region.
XX
KW Her-2/neu; vaccine; cancer; glycoprotein D; cytokine; cytostatic; human;
KW gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004007734-A1.
XX
PD 22-JAN-2004.
XX
PF 15-JUL-2003; 2003WO-KR001400.
XX
PR 16-JUL-2002; 2002KR-00041764.
XX
XX (PANG-) PANGENOMICS CO LTD.
XX
PA
XX
PI Lee JY, Kim D, Chung Y, Chang S, Lee K, Kang C;
XX
XX WPI; 2004-122962/12.
XX
XX New Her-2/neu plasmid construct having anti-cancer activity, useful for
PT preparing a DNA vaccine for preventing and/or treating cancer.
XX
XX Claim 2; SEQ ID NO 2; 70pp; English.
XX
XX The invention relates to an Her-2/neu plasmid construct having anti-
CC cancer activity that is prepared by inserting a truncated human Her-2/neu
CC gene lacking the intracellular domain into plasmid pTV2 or pCK. Aslo
CC provided are a DNA vaccine for preventing and/or treating cancer
CC comprising the plasmid construct and a carrier; and a method for
CC preventing and/or treating cancer by administering the DNA vaccine cited

CC above. The construct is pNeuTM (KCCM-10393), pCKTM (KCCM-10396), pNeuECD
CC (KCCM-10394) or pCKECD (KCCM-10395). The truncated human Her-2/neu gene
CC further lacks the transmembrane domain. The signal peptide of the human
CC Her-2/neu gene is replaced by the signal peptide of herpes simplex type 1
CC glycoprotein D (gp). The plasmid construct is preferably pNeuTM-gDs. The
CC plasmid construct further translates a cytokine gene besides the human
CC Her-2/neu gene. The cytokine gene is selected from granulocyte-macrophage
CC colony-stimulating factor (GM-CSF), FMS-like tyrosine kinase 3 ligand
CC (Flt3L), early T lymphocyte activation-1 (Eta-1), interleukin-12 (IL-12),
CC IL-15 and IL-18. The DNA vaccine further comprises a cytokine gene
CC expressing plasmid. The Her-2/neu plasmid construct is useful for
CC preparing a DNA vaccine for treating and/or preventing cancer. The
CC present sequence represents the nucleotide sequence of the human Her-
CC 2/neu gene lacking the intracellular region.
XX
SQ Sequence 2052 BP; 397 A; 662 C; 601 G; 392 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,05e-10 Length: 2052
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 12 Gaps: 0

US-09-632-036F-6 (1-24) x ADJ57170 (1-2052)

QY 1 ProLeuHisAsnGlnValThrAlaGluAspGlyThrGlnArgAlaGluIysCysSer 20
DB 946 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCACG 1005
QY 21 LysProCysAla 24
DB 1006 AAGCCCTGTGCC 1017

RESULT 17
ADZ47808
ID ADZ47808 standard; DNA; 2061 BP.
XX
AC ADZ47808;
XX
DT 30-JUN-2005 (first entry)
XX
DE DNA encoding human ErbB-2 variant V.
XX
KW epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 151..1995
FT /*tag= a
FT /product= "ErbB-2 variant V"
XX
PN WO2005033133-A2.
XX
PD 14-APR-2005.
XX
PF 04-OCT-2004; 2004WO-US030903.
XX
PR 03-OCT-2003; 2003US-0507953P.
PR 10-NOV-2003; 2003US-0518321P.
PR 09-AUG-2004; 2004US-0599583P.
PR 07-SEP-2004; 2004US-0607326P.
XX
PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
XX
XX Shesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX WPI; 2005-285403/29.
DR

DR P-PSDB; ADZ47809.

XX New isolated polynucleotide encoding at least an active portion of an

PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with

PT aberrant expression or activity of the ErbB-2 polypeptides, such as

PT cancer.

XX Claim 8; SEQ ID NO 15; 246pp; English.

XX The invention relates to the isolation of polynucleotide sequences

CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as

CC HER-2 or neu) polypeptides. Also described are methods, compositions, and

CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and

CC treatment of ErbB-2 related cancer. The sequences, methods, and

CC compositions of the present invention are useful for diagnosing,

CC prognosing, and/or treating diseases or conditions associated with

CC aberrant expression or activity of the ErbB-2 polypeptides, such as

CC cancer. This sequence encodes human ErbB-2 variant V.

XX

SQ Sequence 2061 BP; 392 A; 706 C; 568 G; 395 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,06e-10	Length:	2061
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	14	Gaps:	0

US-09-632-036F-6 (1-24) x ADZ47808 (1-2061)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

Db 1096 CCCCTGCACACCAAGAGGTGCACAGCAGAGTGCACACAGCGGTGTGAGAGTGCAGC 1155

QY 21 LysProCysAla 24

Db 1156 AAGCCCTGTGCC 1167

RESULT 18

ADZ69880

ID ADZ69880 standard; cDNA; 2086 BP.

AC ADZ69880;

XX 14-JUL-2005 (first entry)

XX p185neu oncoprotein-encoding cDNA, SEQ ID 11.

XX gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;

KW vaccine; ss; pharmaceutical.

XX Homo sapiens.

OS Rattus sp.

OS Chimeric.

XX WO2005039618-A1.

XX 06-MAY-2005.

XX 06-OCT-2004; 2004WO-EP011161.

XX 09-OCT-2003; 2003IT-MI001942.

XX (INDE-) INDENA SPA.

XX Amici A, Cavallo F, Fornì G, Marchini C;

XX WPI; 2005-322913/33.

XX New DNA transfer vector containing a sequence coding for a p185neu-fragment, useful for preparing a pharmaceutical composition for treating tumors, and for preparing DNA vaccine.

XX Claim 1; SEQ ID NO 11; 64pp; English.

XX The invention relates to a DNA transfer vector containing a sequence

CC coding for a p185neu-fragment. Also described are: a pharmaceutical

CC composition comprising the DNA vector in admixture with vehicles and

CC excipient; and a combined pharmaceutical preparation containing at least

CC two different plasmids for simultaneous, sequential or separate

CC therapeutic use. The DNA transfer vector is a plasmid, which further

CC contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid

CC is useful in the therapeutic treatment of subjects at risk of developing

CC p185neu positive tumors, or of patients having primary tumors, metastasis

CC or relapses of p185neu-expressing tumors. The plasmid is also useful for

CC the preparation of DNA vaccine. The present sequence represents a p185neu

CC -encoding fragment used in the plasmids of the invention.

XX

SQ Sequence 2086 BP; 405 A; 565 C; 612 G; 404 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,09e-10	Length:	2086
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	14	Gaps:	0

US-09-632-036F-6 (1-24) x ADZ69880 (1-2086)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

Db 977 CCCCTGCACACCAAGAGGTGCACAGCAGAGTGCACACAGCGGTGTGAGAGTGCAGC 1036

QY 21 LysProCysAla 24

Db 1037 AAGCCCTGTGCC 1048

RESULT 19

ADZ69879

ID ADZ69879 standard; cDNA; 2086 BP.

XX ADZ69879;

XX 14-JUL-2005 (first entry)

XX p185neu oncoprotein-encoding cDNA, SEQ ID 10.

XX gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;

KW vaccine; ss; pharmaceutical.

XX Homo sapiens.

OS Rattus sp.

OS Chimeric.

XX WO2005039618-A1.

XX 06-MAY-2005.

XX 06-OCT-2004; 2004WO-EP011161.

XX 09-OCT-2003; 2003IT-MI001942.

XX (INDE-) INDENA SPA.

XX Amici A, Cavallo F, Fornì G, Marchini C;

XX WPI; 2005-322913/33.

XX New DNA transfer vector containing a sequence coding for a p185neu-fragment, useful for preparing a pharmaceutical composition for treating tumors, and for preparing DNA vaccine.

XX Claim 1; SEQ ID NO 10; 64pp; English.

CC The invention relates to a DNA transfer vector containing a sequence
CC coding for a p185neu-fragment. Also described are: a pharmaceutical
CC composition comprising the DNA vector in admixture with vehicles and
CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further
CC contains a CMV transcription promoter and 4 or 8 Cpg motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapses of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.

XX
SQ Sequence 2086 BP; 403 A; 664 C; 615 G; 404 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.09e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69879 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAAACAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAAGTCGAGC 1036

QY 21 LysProCysAla 24

Lb 1037 AAGCCCTGTGCC 1048

RESULT 20

ADZ69881
ID ADZ69881 standard; cDNA; 2086 BP.

XX AC ADZ69881;

XX 14-JUL-2005 (first entry)

XX p185neu oncoprotein-encoding cDNA, SEQ ID 12.

XX gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;
KW vaccine; ss; pharmaceutical.

XX Homo sapiens.

OS Rattus sp.

OS Chimeric.

XX WO2005039618-A1.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further
CC contains a CMV transcription promoter and 4 or 8 Cpg motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapses of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.

XX
SQ Sequence 2086 BP; 410 A; 656 C; 609 G; 411 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.09e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69881 (1-2086)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACAAACAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAAGTCGAGC 1036

QY 21 LysProCysAla 24

Lb 1037 AAGCCCTGTGCC 1048

RESULT 21

ADZ69882

ID ADZ69882 standard; cDNA; 2086 BP.

XX AC ADZ69882;

XX 14-JUL-2005 (first entry)

XX p185neu oncoprotein-encoding cDNA, SEQ ID 13.

XX gene transfer; vector; plasmid; p185neu; cancer; neoplasm; cytostatic;
KW vaccine; ss; pharmaceutical.

XX Homo sapiens.

OS Rattus sp.

OS Chimeric.

XX WO2005039618-A1.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX 06-MAY-2005.

XX New DNA transfer vector containing a sequence coding for a p185neu-
PT fragment, useful for preparing a pharmaceutical composition for treating
PT tumors, and for preparing DNA vaccine.

XX Claim 1; SEQ ID NO 13; 64pp; English.

XX The invention relates to a DNA transfer vector containing a sequence
CC coding for a p185neu-fragment. Also described are: a pharmaceutical
CC composition comprising the DNA vector in admixture with vehicles and
CC excipient; and a combined pharmaceutical preparation containing at least
CC two different plasmids for simultaneous, sequential or separate
CC therapeutic use. The DNA transfer vector is a plasmid, which further

CC contains a CMV transcription promoter and 4 or 8 CpG motifs. The plasmid
CC is useful in the therapeutic treatment of subjects at risk of developing
CC p185neu positive tumors, or of patients having primary tumors, metastasis
CC or relapse of p185neu-expressing tumors. The plasmid is also useful for
CC the preparation of DNA vaccine. The present sequence represents a p185neu
CC -encoding fragment used in the plasmids of the invention.

XX
SQ Sequence 2086 BP; 413 A; 654 C; 608 G; 411 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,09e-10 Length: 2086
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ69882 (1-2086)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 977 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1036

Qy 21 LysProCysAla 24

Db 1037 AAGCCCTGTGCC 1048

RESULT 22

ADG17937
ID ADG17937 standard; DNA; 2132 BP.

XX AC ADG17937;

XX 26-FEB-2004 (first entry)

XX Human HER2-sv form 97 gene encoding sequence.

XX Cytostatic; Gene therapy; HER-2sv polypeptide-related disease; cancer;
KW ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 78..2132
FT /*tag= a

XX WO2003087338-A2.

XX 23-OCT-2003.

XX 11-APR-2003; 2003WO-US011392.

XX 11-APR-2002; 2002US-0371912P.

XX (AMGE-) AMGEN INC.

XX Tatarewicz S, Jing S;

XX WPI; 2003-903161/82.

XX P-PSDB; ADG17938.

XX New-HER-2 splice variant, HER-2sv, nucleic acid molecules, useful for
PT treating, preventing or ameliorating a HER-2sv polypeptide-related
PT disease, condition or disorder, e.g. breast, ovarian, gastric, lung or
PT oral cancer.

XX Claim 1; SEQ ID NO 3; 141pp; English.

XX The present invention relates to a new isolated nucleic acid molecule.
CC The nucleic acid molecule, polypeptide, agent, composition and methods
CC are useful for treating, preventing or ameliorating a HER-2sv polypeptide
CC -related disease, condition or disorder, e.g. cancer, such as breast,
CC ovarian, gastric, lung or oral cancer. The present sequence represents

CC human HER2-sv form 97 gene encoding sequence.
XX
SQ Sequence 2132 BP; 408 A; 692 C; 622 G; 410 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,15e-10 Length: 2132
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 10 Gaps: 0

US-09-632-036F-6 (1-24) x ADG17937 (1-2132)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1023 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1082

Qy 21 LysProCysAla 24

Db 1083 AAGCCCTGTGCC 1094

RESULT 23

ADG17943

ID ADG17943 standard; DNA; 2149 BP.

XX AC ADG17943;

XX 26-FEB-2004 (first entry)

XX Human HER2-sv form 184 gene encoding sequence.

XX Cytostatic; Gene therapy; HER-2sv polypeptide-related disease; cancer;
KW ds.

XX Homo sapiens.

XX Key Location/Qualifiers
FT CDS 1..2145
FT /*tag= a

XX WO2003087338-A2.

XX 23-OCT-2003.

XX 11-APR-2003; 2003WO-US011392.

XX 11-APR-2002; 2002US-0371912P.

XX (AMGE-) AMGEN INC.

XX Tatarewicz S, Jing S;

XX WPI; 2003-903161/82.

XX P-PSDB; ADG17944.

XX New HER-2 splice variant, HER-2sv, nucleic acid molecules, useful for
PT treating, preventing or ameliorating a HER-2sv polypeptide-related
PT disease, condition or disorder, e.g. breast, ovarian, gastric, lung or
PT oral cancer.

XX Claim 1; SEQ ID NO 9; 141pp; English.

XX The present invention relates to a new isolated nucleic acid molecule.
CC The nucleic acid molecule, polypeptide, agent, composition and methods
CC are useful for treating, preventing or ameliorating a HER-2sv polypeptide
CC -related disease, condition or disorder, e.g. cancer, such as breast,
CC ovarian, gastric, lung or oral cancer. The present sequence represents
CC human HER2-sv form 184 gene encoding sequence.

XX SQ Sequence 2149 BP; 414 A; 688 C; 629 G; 418 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.17e-10 Length: 2149
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
Gaps: 0

US-09-632-036F-6 (1-24) x ADG17943 (1-2149)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluIlysCysSer 20
|||
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
|||
Db 1006 AAGCCCTGTGCC 1017

RESULT 24
ADG17939
ID ADG17939 standard; DNA; 2164 BP.
XX
AC ADG17939;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human HER2-sv form 119 gene encoding sequence.
XX
KW Cytostatic; Gene therapy; HER-2sv polypeptide-related disease; cancer;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..2164
FT /*tag= a
XX
PN WO2003087338-A2.
XX
PD 23-OCT-2003.
XX
PF 11-APR-2003; 2003WO-US011392.
XX
PR 11-APR-2002; 2002US-0371912P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Tatarewicz S, Jing S;
XX
DR WPI; 2003-903161/82.
DR P-PSDB; ADG17940.
XX
PT New HER-2 splice variant, HER-2sv, nucleic acid molecules, useful for
PT treating, preventing or ameliorating a HER-2sv polypeptide-related
PT disease, condition or disorder, e.g. breast, ovarian, gastric, lung or
PT oral cancer.
XX
PS Claim 1; SEQ ID NO 5; 141pp; English.
XX
CC The present invention relates to a new isolated nucleic acid molecule.
CC The nucleic acid molecule, polypeptide, agent, composition and methods
CC are useful for treating, preventing or ameliorating a HER-2sv polypeptide
CC -related disease, condition or disorder, e.g. cancer, such as breast,
CC ovarian, gastric, lung or oral cancer. The present sequence represents
CC human HER2-sv form 119 gene encoding sequence.
XX
SQ Sequence 2164 BP; 417 A; 697 C; 625 G; 425 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.19e-10 Length: 2164
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0

DB: 10 Gaps: 0

US-09-632-036F-6 (1-24) x ADG17939 (1-2164)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluIlysCysSer 20
|||
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGATGGAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
|||
Db 1006 AAGCCCTGTGCC 1017

RESULT 25
ADM29355
ID ADM29355 standard; DNA; 2261 BP.
XX
AC ADM29355;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human novel protein NOV20c coding sequence.
XX
KW human; novel protein; NOV; cancer; immune associated disorder; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003064628-A2.
XX
PD 07-AUG-2003.
XX
PF 03-FEB-2003; 2003WO-US003401.
XX
PR 01-FEB-2002; 2002US-0353287P.
PR 01-FEB-2002; 2002US-0353301P.
PR 12-FEB-2002; 2002US-0356371P.
PR 12-FEB-2002; 2002US-0356424P.
PR 13-FEB-2002; 2002US-0356531P.
PR 20-FEB-2002; 2002US-0358239P.
PR 26-FEB-2002; 2002US-0359603P.
PR 27-FEB-2002; 2002US-0359848P.
PR 27-FEB-2002; 2002US-0359860P.
PR 15-MAR-2002; 2002US-0365049P.
PR 22-MAR-2002; 2002US-0366802P.
PR 17-MAY-2002; 2002US-0381666P.
PR 18-JUN-2002; 2002US-0389531P.
PR 19-JUN-2002; 2002US-0389910P.
PR 25-JUN-2002; 2002US-0391516P.
PR 02-JUL-2002; 2002US-0393265P.
PR 07-AUG-2002; 2002US-0401825P.
PR 09-AUG-2002; 2002US-0402395P.
PR 12-AUG-2002; 2002US-0402867P.
PR 23-AUG-2002; 2002US-0405401P.
PR 23-AUG-2002; 2002US-0405820P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Alsobrook JP, Bader JS, Berghs C, Burgess CE, Casman SJ;
PI Catterton E, Chaudhuri A, Edinger SR, Ellerman K, Gerlach VL;
PI Gorman L, Guo X, Herrmann JL, Khramtsov NV, Li L, Miller CE;
PI Ort T, Paturajan M, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
PI Spytek KA, Vernet CAM, Zhong H, Zhong M;
XX
DR WPI; 2003-646149/61.
DR P-PSDB; ADM29356.
XX
PT New NOVX polypeptide, useful for the manufacture of a medicament for
PT treating e.g., cancer or immune associated disorders.
XX
PS Claim 20; SEQ ID NO 99; 606pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC human proteins (NOV proteins). The DNA and protein sequences of the
CC invention are useful for the manufacture of a medicament for treating a

CC syndrome associated with a human disease comprising a pathology
CC associated with the protein, such as: cancer or immune associated
CC disorders. The present DNA sequence encodes a NOV protein of the
CC invention.

XX
SQ Sequence 2261 BP; 451 A; 711 C; 673 G; 426 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,31e-10 Length: 2261
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservativity: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 11 Gaps: 0

US-09-632-036F-6 (1-24) x ADM29355 (1-2261)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
ADZ47794
DB 961 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1020

Qy 21 LysProCysAla 24
DB 1021 AAGCCCTGTGCC 1032

RESULT 26
ADZ47794
ID ADZ47794 standard; DNA; 2320 BP.
XX
AC ADZ47794;
XX
DT 30-JUN-2005 (first entry)
XX
DE DNA encoding human ErbB-2 variant I.
XX
KW epidermal growth factor receptor-2; ErbB-2; HER-2; neu; diagnosis;
KW prognosis; cancer; cytostatic; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 151..2187
FT /*tag= a
FT /product= "ErbB-2 variant I"
FT CDS 2097..2320
FT /*tag= b
FT /product= "Active region of ErbB-2 variant I"
FT /note= "Given as SEQ ID No:7, specifically claimed in
FT Claim 5"
XX
PN WO200503133-A2.
XX
PD 14-APR-2005.
XX
PF 04-OCT-2004; 2004WO-US030903.
XX
PR 03-OCT-2003; 2003US-0507953P.
PR 10-NOV-2003; 2003US-0518321P.
PR 09-AUG-2004; 2004US-059583P.
PR 07-SEP-2004; 2004US-0607326P.
XX
PA (COMP-) COMPUEN LTD.
PA (COMP-) COMPUEN INC.
XX
PI Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX
DR WPI; 2005-285403/29.
DR P-PsDB; ADZ47795.
XX
PT New isolated polynucleotide encoding at least an active portion of an
PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
PT aberrant expression or activity of the ErbB-2 polypeptides, such as

PT cancer.
PS Claim 3; SEQ ID NO 1; 246pp; English.
XX
CC The invention relates to the isolation of polynucleotide sequences
CC encoding novel epidermal growth factor receptor-2 (ErbB-2, also known as
CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
CC treatment of ErbB-2 related cancer. The sequences, methods, and
CC compositions of ErbB-2 related cancer. The sequences, methods, and
CC prognosing, and/or treating diseases or conditions associated with
CC aberrant expression or activity of the ErbB-2 polypeptides, such as
CC cancer. This sequence encodes human ErbB-2 variant I.
XX
SQ Sequence 2320 BP; 448 A; 771 C; 673 G; 428 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,38e-10 Length: 2320
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservativity: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036F-6 (1-24) x ADZ47794 (1-2320)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
ADZ47794
DB 1096 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155

Qy 21 LysProCysAla 24
DB 1156 AAGCCCTGTGCC 1167

RESULT 27
AAT72725
ID AAT72725 standard; cDNA; 2385 BP.
XX
AC AAT72725;
XX
DT 17-SEP-1997 (first entry)
XX
DE Her2-GM-CSF immunostimulant fusion protein DNA.
XX
KW Her2-GM-CSF; granulocyte macrophage colony stimulating factor;
KW growth factor receptor; oncogene; immunostimulant; cancer; therapy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 11..2359
FT /*tag= a
FT /product= "GM-CSF-Her2 fusion protein"
FT mRNA 11..1969
FT /*tag= b
FT /product= "Her2"
FT mRNA 1970..1975
FT /*tag= c
FT /product= "Leu-Glu linker"
FT mRNA 1976..2359
FT /*tag= d
FT /product= "GM-CSF"
XX
PN WO9724438-A1.
XX
PD 10-JUL-1997.
XX
PF 23-DEC-1996; 96WO-US020241.
XX
PR 28-DEC-1995; 95US-00579823.
XX
PA (ACTI-) ACTIVATED CELL THERAPY INC.
XX

PI Laus R, Ruegg CL, Wu H;
XX WPI; 1997-363674/33.
DR P-PSDB; AAW19764.
XX
XX Potent APC that activates T-cells to give multivalent cellular immune
PT response - can also induce a cytotoxic T-cell response in a vertebrate
PT subject.
XX
XX Disclosure; Fig 8; 45pp; English.
PS
XX A nucleic acid molecule (AAT72725) codes for a fusion protein (AAW19764)
CC comprising granulocyte-macrophage colony stimulating factor (GM-CSF) and
CC Her2, a growth factor receptor that is over-expressed in breast and
CC ovarian cancer cells. It was prep'd. by PCR amplification of Her2 cDNA
CC from a breast cancer cell line and fusion to GM-CSF cDNA. Fusion
CC expression vectors can be used to transfect mammalian and insect cells.
CC The Her2-GM-CSF fusion protein is used to generate anti-Her2 immunity.
CC Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo
CC or in vitro by exposure to antigen-presenting cells exposed to the fusion
CC protein.
XX
SQ Sequence 2385 BP; 488 A; 780 C; 677 G; 440 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,46e-10 Length: 2385
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036f-6 (1-24) x AAT72725 (1-2385)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 956 CCCTGTCACCAACCAAGAGGTGACAGCAGAGGATGGAAACACACGCGGTGTGAGAAAGTGCAGC 1015

QY 21 LysProCysAla 24
DB 1016 AAGCCCTGTGCC 1027

RESULT 28
ADZ47806
ID ADZ47806 standard; DNA; 2437 BP.
XX
AC ADZ47806;
XX
XX 30-JUN-2005 (first entry)
XX
XX DNA encoding human ErbB-2 variant IV.
XX
XX epidermal growth factor receptor-2; ErbB-2; neu; diagnosis;
KW prognosis; cancer; cytostatic; gene; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH CDS 151..2304
FT /*tag= a
FT /product= "ErbB-2 variant IV"
XX
XX WO200503133-A2.
XX
XX 14-APR-2005.
XX
XX 04-OCT-2004; 2004WO-US030903.
XX
XX 03-OCT-2003; 2003US-0507953P.
PR 10-NOV-2003; 2003US-0518321P.
PR 09-AUG-2004; 2004US-0599583P.
PR 07-SEP-2004; 2004US-0607326P.
XX

PA (COMP-) COMPUGEN LTD.
PA (COMP-) COMPUGEN INC.
XX
XX Shemesh R, Oren A, Rotman G, Sela-Tavor O, Walach S;
PI Sameach-Greenwald S, Beiman M, Eshel D, Savitsky K;
XX
XX WPI; 2005-285403/29.
DR P-PSDB; ADZ47807.
XX
XX New isolated polynucleotide encoding at least an active portion of an
PT ErbB-2 polypeptide, useful for diagnosing or treating diseases with
PT aberrant expression or activity of the ErbB-2 polypeptides, such as
PT cancer.
XX
XX Claim 3; SEQ ID NO 13; 246pp; English.
PS
XX The invention relates to the isolation of polynucleotide sequences
CC encoding novel epidermal growth factor receptor-2 (ErbB-2), also known as
CC HER-2 or neu) polypeptides. Also described are methods, compositions, and
CC kits using the novel ErbB-2 sequences for the diagnosis, prognosis, and
CC treatment of ErbB-2 related cancer. The sequences, methods, and
CC compositions of the present invention are useful for diagnosing,
CC prognosing, and/or treating diseases or conditions associated with
CC aberrant expression or activity of the ErbB-2 polypeptides, such as
CC cancer. This sequence encodes human ErbB-2 variant IV.
XX
SQ Sequence 2437 BP; 470 A; 806 C; 702 G; 459 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,53e-10 Length: 2437
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 14 Gaps: 0

US-09-632-036f-6 (1-24) x ADZ47806 (1-2437)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 1096 CCCCTGTCACCAACCAAGAGGTGACAGCAGAGGATGGAAACACACGCGGTGTGAGAAAGTGCAGC 1155

QY 21 LysProCysAla 24
DB 1156 AAGCCCTGTGCC 1167

RESULT 29
ADT50728
ID ADT50728 standard; DNA; 2802 BP.
XX
AC ADT50728;
XX
XX 13-JAN-2005 (first entry)
XX
XX Cancer related nucleic acid sequence #32.
DE
XX ds; gene; cytostatic; gene therapy; vaccine; diagnosis; breast; colon;
KW lung; ovarian; prostate; cancer.
XX
XX Homo sapiens.
XX
XX WO2004092338-A2.
XX
XX 28-OCT-2004.
XX
XX 12-APR-2004; 2004WO-US011104.
XX
XX 11-APR-2003; 2003US-0462399P.
PR 01-JUL-2003; 2003US-0484333P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Macina RA, Turner LR, Sun Y, Tam A;
PI

```

XX WPI; 2004-766851/75.
DR
XX New cancer specific nucleic acid (CaSNA) molecules, useful for
PT diagnosing, monitoring the presence of, or treating a patient with
PT breast, colon, lung, ovarian, or prostate cancer.
XX
PS Claim 1; SEQ ID NO 32; 891pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I)
CC selectively hybridizing to, or comprising at least 95% sequence identity
CC to, any of the 362 nucleotide sequences fully defined in the
CC specification. The nucleic acid molecules and polypeptides are useful for
CC diagnosing, monitoring the presence of, or treating a patient with
CC breast, colon, lung, ovarian, or prostate cancer. This sequence
CC corresponds to a nucleic acid of the invention.
XX
SQ Sequence 2802 BP; 567 A; 859 C; 843 G; 532 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 3e-10 Length: 2802
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 13 Gaps: 0

US-09-632-036F-6 (1-24) x ADT50728 (1-2802)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCCTGCACACCAAGAGGTGCACAGCAGGATGCACACACAGCGTGTGAGAAGTGCAGC 1155

Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 30
AAZ50586
ID AAZ50586 standard; DNA; 2871 BP.
XX
AC AAZ50586;
XX
DT 23-MAY-2000 (first entry)
XX
DE DC8scFv-erbB2EC fusion construct: containing tetramerisation domain.
XX
KW DC8 scFv; single-chain variable fragment; erbB2EC; extracellular domain;
KW human; fusion construct; tetramerisation domain; constant domain;
KW heteroinibody; multifunctional compound; melanoma; sarcoma;
KW immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; ds.
XX
OS Unidentified.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT CDS 10..2865
FT /*tag= a
FT /product= "DC8scFv-erbB2EC fusion protein"
FT sig_peptide 10..66
FT /*tag= b
FT /label= Leader_sequence
FT misc_feature 67..390
FT /*tag= c
FT /label= DC8scFv_light_chain_variable_region
FT misc_feature 391..435
FT /*tag= d
FT /label= Glycine-Serine-linker_DNA
FT misc_feature 436..771
FT /*tag= e

```

```

FT misc_feature /label= DC8scFv_heavy_chain_variable_region
FT 775..807
FT /*tag= f
FT /note= "5' end of human IgG3 upper hinge region with 3
FT additional nucleotides"
FT 808..924
FT /*tag= g
FT /label= Human_p53_tetramerisation_domain
FT 925..945
FT /*tag= h
FT /label= Short_peptide_linker
FT 946..2844
FT /*tag= i
FT /label= erbB2EC_domain
FT 2845..2862
FT /*tag= j
FT /label= His_tag
XX
XX WO200006605-A2.
XX
XX 10-FEB-2000.
XX
XX 28-JUL-1999; 99WO-EP005416.
XX
XX 28-JUL-1998; 98EP-00114082.
XX
XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
XX Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX WPI; 2000-195265/17.
DR
DR P-PSDB; AAY44993.
XX
XX New multifunctional compounds useful for preventing and/or treating
XX malignant cell growth and for detection and diagnosis.
XX
XX Example 9; Fig 49; 166pp; English.
XX
CC The patent discloses heteroinibodies which are multifunctional compounds
CC producible in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heteroinibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a fusion construct
CC comprising DC8 single-chain Fv (scFv) fragment at the N-terminus,
CC extracellular domain of human erbB2 at the C-terminus and a
CC tetramerisation domain between them. This construct was prepared to find
CC out whether an oligomerisation domain characterised in bacterial
CC expression system is applicable for expression of fully functional and
CC secretable recombinant protein in mammalian host cells. This tetrameric
CC construct was not expressed as secretable and fully functional protein in
CC mammalian cells. Hence general applicability of the tetramerisation
CC domain for oligomerisation strategies in mammalian cells was ruled out
XX
SQ Sequence 2871 BP; 598 A; 868 C; 834 G; 571 T; 0 U; 0 Other;

```

```

Alignment Scores:
Pred. No.: 3.09e-10 Length: 2871
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

```



```
CC immune response to the HER-2/neu protein. It may be used to treat
CC malignancies such as breast, ovarian, colon, lung and prostate cancers,
CC and may be used as an antigen to vaccinate against these neoplasias
XX
SQ Sequence 3600 BP; 723 A; 1108 C; 1075 G; 694 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.08e-10 Length: 3600
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x AAA89736 (1-3600)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 33
ID ABK86207 standard; cDNA; 3678 BP.
XX
AC ABK86207;
XX
DT 24-SEP-2002 (first entry)
XX
DE cDNA encoding human breast cancer antigen, Her2 variant.
XX
KW Human; Her2; cytostatic; antiviral; immunostimulant;
KW cell-mediated immune response; tumour; breast cancer; virus infection;
KW prostate cancer; colorectal cancer; pancreatic cancer; lymphoma;
KW leukaemia; hepatitis virus; lentivirus; herpesvirus;
KW human immunodeficiency virus; HIV; flavivirus; pestivirus; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..3678
FT /tag= a
FT /product= "Breast cancer antigen Her2 variant"
XX
PN WO200240059-A2.
XX
PD 23-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045626.
XX
PR 01-NOV-2000; 2000US-00704232.
XX
PA (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
PA (MINC/) MINCHEFF M S.
PA (LOUK/) LOUKINOV D I.
PA (ZOUR/) ZOURAK S.
XX
PI Mincheff MS, Loukinov DI, Zoubak S;
XX
DR WPI; 2002-527524/56.
XX
DR P-PSDB; AAU98923.
XX
PT Inducing a cell-mediated immune response against a target antigen,
PT reducing undesired cells and stimulating presentation of an antigen by a
PT cell, comprises administering a polynucleotide encoding a variant of an
PT antigen.
XX
PS Disclosure; Page 128-134; 146pp; English.
XX
PT The invention relates to a method of inducing a cell-mediated immune
```

```
CC response against a cell comprising a target antigen (I) in a subject,
CC treating a subject having undesired cells, for example tumour cells or
CC virally infected cells (C), reducing the number of (C) in a subject, and
CC stimulating presentation of (I) by a cell. This is done by administering
CC a polynucleotide (II) encoding a variant of (I), so that (II) expressed
CC in a cell and cell-mediated immune response is induced. The method can be
CC used to treat prostate cancer, breast cancer, colorectal cancer and
CC pancreatic cancer, as well as lymphomas and leukaemias. The method is
CC also useful in treating chronic viral infections such as those caused by
CC hepatitis viruses, lentiviruses (including human immunodeficiency virus
CC (HIV)), herpesviruses and the flaviviruses and pestiviruses. The present
CC sequence represents the coding sequence of human breast cancer antigen,
CC Her2 variant, used as a target antigen in the method of the invention
XX
SQ Sequence 3678 BP; 746 A; 1137 C; 1091 G; 704 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.19e-10 Length: 3678
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x ABK86207 (1-3678)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 856 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCGC 915
Qy 21 LysProCysAla 24
Db 916 AAGCCCTGTGCC 927

RESULT 34
ID ADB67620 standard; DNA; 3765 BP.
XX
AC ADB67620;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human epidermal growth factor receptor 2 coding sequence.
XX
KW ds; gene; cytostatic; human epidermal growth factor receptor-3; HER-3;
KW heregulin; HER2; tyrosine kinase activity; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..3765
FT /tag= a
FT /product= "Human epidermal growth factor receptor 2"
FT /note= "no stop codon given at the 3' end"
XX
PN WO2003011897-A1.
XX
PD 13-FEB-2003.
XX
PF 29-JUL-2002; 2002WO-US023963.
XX
PR 27-JUL-2001; 2001US-0308341P.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Singer E, Landgraf R, Slamon DJ, Eisenberg D;
XX
DR WPI; 2003-300482/29.
XX
DR P-PSDB; ADB67621.
XX
PT Novel human epidermal growth factor receptor 3 variant as agonist or
PT antagonist of HER3 receptor, for diagnosis/treatment of cells or
PT pathological conditions associated with aberrant expression of heregulin
```

PT or HER3.
XX
PS Disclosure; Page 80-81; 137pp; English.
XX
CC The invention relates to a non-naturally occurring human epidermal growth
CC factor receptor (HER)-3 variant polypeptide comprising amino acids 19-329
CC or 20-329 of the 1342 amino acid HER3 polypeptide (ADB67617) or a
CC sequence which differs from native HER3 polypeptide and having amino acid
CC substitutions at residues E43, N44, K51, E64, V66 and V110 of S1, is new.
CC The variant HER-3 specifically binds to the heregulin polypeptide
CC (ADB67619), exhibits an impaired ability to interact with HER2
CC polypeptide (ADB67621), or has an ability to inhibit the interaction
CC between wild-type HER3 and heregulin. The polypeptide is useful for
CC identifying a compound which specifically binds to heregulin binding
CC domain in a HER3 variant polypeptide. The method further involves
CC determining whether the test compound inhibits or enhances the heregulin
CC induced tyrosine kinase activity associated with a HER3 polypeptide. The
CC polypeptide is also useful for determining whether a test compound
CC modulates the interaction between a heregulin polypeptide, and the
CC variant HER-3 polypeptide. The HER-3 polypeptide is also useful for
CC inhibiting the interaction between a heregulin polypeptide and HER3
CC polypeptide, e.g. for treating cancer. The polypeptide is also useful for
CC stimulating or activating HER3 receptor. This sequence represents the
CC coding sequence for the wild type human HER-2 polypeptide.
XX
SQ Sequence 3765 BP; 757 A; 1170 C; 1120 G; 718 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,31e-10	Length:	3765
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	10	Gaps:	0

US-09-632-036F-6 (1-24) x ADB67620 (1-3765)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 946 CCCTTGACACCAACAGAGGTGACAGCAGAGGATGGACACAGCGGTGTGAGAGTGCAGC 1005

QY 21 LysProCysAla 24

DB 1006 AAGCCCTGTGCC 1017

RESULT 35

ADZ72379

ID ADZ72379 standard; cDNA; 3765 BP.

AC ADZ72379;

DT 14-JUL-2005 (first entry)

XX DNA encoding human epidermal growth factor receptor-2, HER2.

DE Aptamer; epidermal growth factor receptor-2; HER2; tumor; drug screening;
KW cancer; cytostatic; diagnosis; carcinoma; lymphoma; sarcoma; leukemia;
KW ss; gene.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..3765

FT FT /*tag= a

FT FT /product= "HER2"

XX WO2005040339-A2.

XX 06-MAY-2005.

XX 16-JUL-2004; 2004WO-US023039.

XX 18-JUL-2003; 2003US-0488679P.

XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Chen CB, Landgraf R;
XX
DR WPI; 2005-333498/34.
DR P-PSDB; ADZ72380.
XX
PT New aptamers to human epidermal growth factor receptor-3, useful for
PT diagnosing, treating or preventing cancer, e.g. carcinoma, lymphoma,
PT blastoma, sarcoma, and leukemia.
PT
XX Disclosure; SEQ ID NO 5; 74pp; English.
XX
CC The present invention relates to compositions of nucleic acid aptamers
CC that bind to human epidermal growth factor receptor-3 (HER3) comprising
CC the protein sequence given as SEQ ID NO: 2 (see ADZ72376). HER3 is a
CC receptor tyrosine kinase which are involved in a broad spectrum of cell
CC growth and differentiation events. Overexpression of members of this
CC receptor family such as epithelial growth factor receptor and, HER3 and
CC HER2, is associated with a variety of solid tumor malignancies. SELEX
CC (Systematic Evolution of Ligands by Exponential enrichment), was used to
CC select RNA aptamers against the oligomeric states of the extracellular
CC domains (ECD) of HER3. A number of specific RNA aptamers and methods of
CC making these aptamers are disclosed. One of the aptamers, A30 binds with
CC high affinity to a limited number of binding sites in the oligomeric
CC state of HER3ECD. High affinity binding of A30 inhibits heregulin-
CC dependent tyrosine phosphorylation of HER2 as well as heregulin induced
CC growth of MCF7 cells. This aptamer can be useful as a tool for analysis
CC of receptor interactions and may serve as a lead compound for the
CC development of inhibitors against overexpressed receptor tyrosine kinases
CC in pathologies associated with HER3 overexpression, such as cancer.
CC Disclosed is one such aptamer given as SEQ ID NO: 19 (see ADZ72393),
CC others comprise SEQ ID NOS: 7, 12, 15-18. The aptamers further comprise a
CC fluorine moiety or an amino moiety. They form a hairpin loop structure
CC and further comprise a stem structure comprised of at least 1-6 base
CC pairs. Also disclosed a nucleic acid (SEQ ID NO:1) encoding a HER3
CC polypeptide. The nucleic acid, a composition, and an analysis method are
CC useful for diagnosing, treating or preventing cancer, e.g. carcinoma,
CC lymphoma, blastoma, sarcoma, and leukemia. The present sequence is a DNA
CC sequence encoding HER2.
XX
SQ Sequence 3765 BP; 757 A; 1170 C; 1120 G; 718 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4,31e-10	Length:	3765
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	14	Gaps:	0

US-09-632-036F-6 (1-24) x ADZ72379 (1-3765)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 946 CCCTTGACACCAACAGAGGTGACAGCAGAGGATGGACACAGCGGTGTGAGAGTGCAGC 1005

QY 21 LysProCysAla 24

DB 1006 AAGCCCTGTGCC 1017

RESULT 36

AAT40739

ID AAT40739 standard; cDNA; 3768 BP.

XX AAT40739;

XX 01-JAN-1997 (first entry)

XX HER-2/neu oncogene.

XX HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;

KW breast cancer; ovary cancer; colon cancer; lung cancer; prostate cancer;
KW genetic immunisation; tumour; vaccine; vector; ss.
XX Homo sapiens.

OS
FH Key Location/Qualifiers
CDS 1..3765
FT /*tag= b
FT /note= "nucleotides 2026-3765 (claim 1) code for HER-
FT 2/neu intracellular domain"
XX

XX W09J0514 AL.
XX
XX
PD 03-OCT-1996.
XX
XX
XX 28-MAR-1996; 96WO-US001689.
XX
XX 31-MAR-1995; 95US-00414417.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Cheever MA, Disis ML;
XX
XX WPI; 1996-455361/45.
XX P-PSDB; AAW01111.
XX

XX DNA encoding HER-2/neu poly:peptide(s) - used for prevention or treatment
XX of malignancies with which the HER-2/neu oncogene is associated.
XX
XX
XX Claim 1; Page 49-56; 71pp; English.
XX

XX Human HER-2/neu oncogene cDNA (AAT40739) codes for HER-2/enu (p185 or c-
XX erbB2) protein (AAW01111). The oncogene is overexpressed in various
XX cancers, including breast, ovarian, colon, lung and prostate, and appears
XX to induce malignancies through quantitative mechanisms that result from
XX increased or deregulated expression of an essentially normal gene
XX product. Nucleotides 2026-3765 of the cDNA sequence code for the
XX intracellular domain (Lys676-Val1255) of the HER-2/neu protein, which is
XX useful for immunisation against malignancy. Nucleic acids can be used to
XX direct expression of the intracellular domain in transformed host cells,
XX or are used, alone or in a viral vector, for genetic immunisation of an
XX animal
XX

XX
SQ Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.32e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x AAT40739 (1-3768)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACGCGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 37

AAAX01912

ID AAX01912 standard; DNA; 3768 BP.

XX AAX01912;

XX 21-APR-1999 (first entry)

XX Human HER-2/neu oncogene DNA.

XX
XX
XX

KW HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;
KW malignancy; treatment; tumour; ss.
XX Homo sapiens.

OS
FH Key Location/Qualifiers
CDS 1..3768
FT /*tag= a
FT /product= "HER-2/neu"
FT /note= "oncogene"
FT 2026..3765
FT misc_feature
FT /*tag= b
FT /note= "region which elicits immune response"
XX

XX US5869445-A.
XX
XX 09-FEB-1999.
XX
XX 01-APR-1996; 96US-00625101.
XX
XX 17-MAR-1993; 93US-00033644.
XX 12-AUG-1993; 93US-00106112.
XX 31-MAR-1995; 95US-00414417.
XX
XX (UNIW) UNIV WASHINGTON.
XX

XX Cheever MA, Disis ML;
XX
XX WPI; 1999-152835/13.
XX P-PSDB; AAW92406.
XX

XX Use of HER-2/neu polypeptides - for eliciting an immune response to an
XX HER-2/neu associated malignancy, particularly for treating or preventing
XX tumours.
XX Claim 1a; Col 23-32; 26pp; English.
XX
XX This sequence encodes the human HER-2/neu oncogene protein. A fragment of
XX this protein is used in a method for eliciting or enhancing an immune
XX response to HER-2/neu protein. The polypeptide can stimulate T cells and
XX B cells to produce an immune response to the HER-2/neu protein. The
XX method can be used for immunisation against a malignancy in which the HER
XX -2/neu oncogene is associated and in the treatment of an existing tumour,
XX or to prevent tumour occurrence or reoccurrence
XX
XX
SQ Sequence 3768 BP; 759 A; 1171 C; 1119 G; 719 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.32e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x AAX01912 (1-3768)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACGCGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 38

AAA09455

ID AAA09455 standard; DNA; 3768 BP.

XX AAA09455;

XX 10-AUG-2000 (first entry)

XX
XX
XX

Mon Dec 12 11:36:45 2005

```

XX RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
KW virucide; protozoacide; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200255693-A2.
XX
PD 18-JUL-2002.
XX
PF 09-JAN-2002; 2002WO-EP000152.
XX
PR 09-JAN-2001; 2001DE-01000586.
PR 26-OCT-2001; 2001DE-01055280.
PR 29-NOV-2001; 2001DE-01058411.
PR 07-DEC-2001; 2001DE-01060151.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;
XX
XX WPI; 2002-590671/63.
XX
PT Inhibiting expression of target gene, useful e.g. for inhibiting
PT oncogenes, by administering double-stranded RNA complementary to the
PT target and having an overhang.
XX
PS Claim 10; Page 142-143; 203pp; German.
XX
CC The invention relates to inhibiting expression of a target gene (I) in a
CC cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded
CC structure of at most 49 consecutive bases. At least part of one strand
CC (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.
CC in humans, also genes in Plasmodium or in viruses or viroids that are
CC pathogenic for humans, animals or plants. Introducing an overhang into
CC dsRNA greatly increases effectiveness for inhibiting gene expression,
CC both in vivo and in vitro and also increases stability and thus the
CC effective concentration inside the cell. The present sequence is that of
CC a gene related to the invention
XX
SQ Sequence 3768 BP; 758 A; 1170 C; 1121 G; 719 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.32e-10 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x ABV78168 (1-3768)
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Db 946 CCCCTGCACCAACCAAGAGGTGACAGAGGATGACAGAGGATGACAGCGGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

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Search completed: December 10, 2005, 22:51:49
Job time : 297.091 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 22:40:44 ; Search time 93.8182 Seconds
(without alignments)
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Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHNOEVTABDGTQAEKSKPCA 24

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Fgapop 6.0 , Fgapext 7.0
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Searched: 1303057 seqs, 888780828 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	128	97.0	2385	3	US-08-579-823A-3
5	128	97.0	2385	3	US-09-344-195-3
6	128	97.0	3768	2	US-08-625-101-1
7	128	97.0	3768	2	US-08-356-786-1
8	128	97.0	3768	3	US-09-811-115-2
9	128	97.0	3768	3	US-09-167-516-1
10	128	97.0	4473	2	US-09-048-804-1
11	128	97.0	4473	3	US-09-056-105-26
12	128	97.0	4473	3	US-09-663-83A-3
13	128	97.0	4473	3	US-09-441-411-5
14	128	97.0	4530	2	US-08-229-515A-9
15	128	97.0	4530	2	US-08-645-865-9
16	128	97.0	4530	3	US-09-167-322-4
17	128	97.0	4530	3	US-09-527-487-1
18	128	97.0	4530	3	US-09-877-177A-11
19	128	97.0	9274	3	US-09-811-115-1
20	114	86.4	3955	2	US-08-229-515A-14
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22	54	40.9	601	3	US-09-949-016-195823
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25	53.5	40.5	1288	3	US-09-270-767-232
26	53.5	40.5	1288	3	US-09-270-767-15514
27	52	39.4	471	3	US-09-235-451-10
28	52	39.4	471	3	US-09-978-303-10
29	52	39.4	1062	3	US-09-902-540-6754
30	52	39.4	1318	2	US-08-809-494A-5
31	52	39.4	1318	3	US-09-352-302-5
32	52	39.4	2637	3	US-09-949-016-5623
33	52	39.4	3707	3	US-09-902-540-549
34	52	39.4	6975	3	US-09-902-540-2386
35	52	39.4	17315	3	US-09-902-540-1103
36	52	39.4	27227	3	US-09-949-016-17365
37	52	39.4	141248	3	US-09-949-016-12241
38	52	39.4	143248	3	US-09-949-016-16652
39	51	38.6	1763	3	US-09-385-219A-13
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43	50	37.9	2236	3	US-09-697-367-1
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56	49	37.1	458	3	US-09-270-767-16225
57	49	37.1	532	3	US-09-902-540-1555
58	49	37.1	1593	3	US-09-676-610B-25
59	49	37.1	1868	2	US-08-658-883B-1
60	49	37.1	1868	3	US-09-676-610B-26
61	49	37.1	2801	3	US-09-291-922-7
62	49	37.1	3633	2	US-09-715-249-1
63	49	37.1	5532	2	US-08-475-035-3
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Qy	21	LysProCysAla	24		
Db	943	AAGCCCGUGCC	954		

RESULT 3

US-09-146-283-3
 ; Sequence 3, Application US/09146283
 ; Patent No. 5976546
 ; GENERAL INFORMATION:
 ; APPLICANT: Laus, Reiner
 ; APPLICANT: Ruegg, Curtis L.
 ; APPLICANT: Wu, Hongyu
 ; TITLE OF INVENTION: Immunostimulatory Compositions
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dehlinger & Associates
 ; STREET: 350 Cambridge Ave. Suite 250
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94306
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/146,283
 ; FILING DATE: 03-SEPT-1998
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:

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	Best Local Similarity:	95.83%	Mismatches:	1
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US-09-632-036F-6 (1-24) x US-09-146-283-3 (1-2385)

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Qy	21	LysProCysAla	24
Db	1016	AAGCCCTGTGCC	1027

RESULTS

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US-08-579-823A-3
: Sequence 3, Application US/08579823A
: Patent No. 6080409
: GENERAL INFORMATION:
: APPLICANT: Laus, Reiner
: APPLICANT: Ruegg, Curtis L.
: APPLICANT: Wu, Hongyu
: TITLE OF INVENTION: Immunostimulatory Composition and Method
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Ave. Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/579,823A
: FILING DATE: 03-DEC-1998
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Judge, Linda R.
: REGISTRATION NUMBER: 42,702
: REFERENCE/DOCKET NUMBER: 7636-0010
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-324-0880
: TELEFAX: 650-324-0960
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2385 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: homo sapiens
: INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
US-08-579-823A-3

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Best Local Similarity:	95.83%	Mismatches: 1
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RESULT 5

US 09-344-195-3
; Sequence 3, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laue, Reiner
; Ruegg, Curtis L.
; Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Denlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; (CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSP-HER-2 fusion gene; Fig. 8
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-344-195-3

Alignment Scores:

Pred. No.:	5.87e-10	Length:	2385
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Best Local Similarity:	95.83%	Mismatches:	1
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US-09-632-036F-6 (1-24) x US-09-344-195-3 (1-2385)

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Db	1016	AAGCCCTGTGCC	1027

RESULT 6

US-08-625-101-1
; Sequence 1, Application US/08625101
; Patent No. 5869445

; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
; TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
; TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
; TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/625,101
; FILING DATE: 01-APR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..3765
; US-08-625-101-1

Alignment Scores:

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Db	1006	AAGCCCTGTGCC	1017

RESULT 7

US-08-356-786-1
; Sequence 1, Application US/08356786
; Patent No. 5877305

; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3768
OTHER INFORMATION: /note= "product = "cerB-b2""
US-08-356-786-1

Alignment Scores:
Pred. No.: 1e-09 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x US-08-356-786-1 (1-3768)

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Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGAGTGGAAACACAGCGGTGTGAGAGTGCAGC 1005

Oy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 8

Sequence 2, Application US/09811115
Patent No. 6632979
GENERAL INFORMATION:
APPLICANT: Erickson, Sharon
APPLICANT: Schwall, Ralph
APPLICANT: King, Kathleen
TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
FILE REFERENCE: GENENT.034A
CURRENT APPLICATION NUMBER: US/09/811,115
CURRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/189,844
PRIOR FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 2

LENGTH: 3768
TYPE: DNA
ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 1e-09 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-811-115-2 (1-3768)

Oy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGACAGCAGAGAGTGGAAACACAGCGGTGTGAGAGTGCAGC 1005
Oy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 9

US-09-167-516-1
Sequence 1, Application US/09167516
Patent No. 6953573
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
TITLE OF INVENTION: ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/167,516
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3768 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..3765
US-09-167-516-1

Alignment Scores:

```
Pred. No.: 1e-09 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-167-516-1 (1-3768)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||||
Db 946 CCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGC 1005
|||||

QY 21 LysProCysAla 24
|||||
Db 1006 AAGCCCTGTGCC 1017
|||||

RESULT 10
US-09-048-804-1
; Sequence 1, Application US/09048804
; Patent No. 5968748
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett, Allan Lipton, Lois M. Witters
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION OF
; HUMAN HER-2 EXPRESSION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5968748ris LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,804
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legaard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: ISIS-2913
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4473 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; ANTI-SENSE: NO
US-09-048-804-1

Alignment Scores:
Pred. No.: 1.22e-09 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-048-804-1 (1-4473)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||||
Db 1120 CCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGC 1179
|||||

QY 21 LysProCysAla 24
|||||
Db 21 LysProCysAla 24
|||||
Db 1180 AAGCCCTGTGCC 1191
|||||

RESULT 12
US-09-663-834A-3
; Sequence 3, Application US/09663834A
; Patent No. 6613567
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowbert
; TITLE OF INVENTION: ANTISENSE MODULATION OF HER-2 EXPRESSION
; FILE REFERENCE: RTS-0033
; CURRENT APPLICATION NUMBER: US/09/663,834A
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 48
; SEQ ID NO 3
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175) ... (3942)
US-09-663-834A-3

Alignment Scores:
Pred. No.: 1.22e-09 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-663-834A-3 (1-4473)
```


Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-877-177A-11 (1-4530)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAepGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 19

US-09-811-115-1
; Sequence 1, Application US/09811115
; Patent No. 6632979
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811.115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9274
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector Sequence
US-09-811-115-1

Alignment Scores:
Pred. No.: 2,85e-09 Length: 9274
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-811-115-1 (1-9274)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAepGlyThrGlnArgAlaGluLysCysSer 20
Db 2676 CCCCTGCACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 2735
Qy 21 LysProCysAla 24
Db 2736 AAGCCCTGTGCC 2747

RESULT 20

US-08-229-515A-14
; Sequence 14, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3955 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-229-515A-14

Alignment Scores:
Pred. No.: 1,44e-07 Length: 3955
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x US-08-229-515A-14 (1-3955)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAepGlyThrGlnArgAlaGluLysCysSer 20
Db 974 CCCCCGAATAACCAAGAGGTGACAGCTGAGGACGGAACACACAGCGTTGTGTGAGAAATGCAGC 1033
Qy 21 LysProCysAla 24
Db 1034 AAGCCCTGTGCT 1045

RESULT 21

US-08-645-865-14
; Sequence 14, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:

```
/ ; TELEPHONE: 404-688-0770
/ ; TELEFAX: 404-688-9880
/ ; INFORMATION FOR SEQ ID NO: 14:
/ ; SEQUENCE CHARACTERISTICS:
/ ; LENGTH: 3955 base pairs
/ ; TYPE: nucleic acid
/ ; STRANDEDNESS: single
/ ; TOPOLOGY: linear
US-08-645-865-14

Alignment Scores:
Pred. No.: 1.44e-07 Length: 3955
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x US-08-645-865-14 (1-3955)
>Y 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 974 CCCCCGAATACCAAGAGGTACAGCTGAGGACGGAACACAGCGTTGTGAGAAATGCAGC 1033

Qy 21 LysProCysAla 24
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1034 AAGCCCTGTGCT 1045

RESULT 22
US-09-949-016-195823
; Sequence 195823, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195823
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-195823

Alignment Scores:
Pred. No.: 22.6 Length: 601
Score: 54.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 40.91% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-949-016-195823 (1-601)
Qy 5 GlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 391 CAGGAGCTCACAGCTGAGATGGGTTTCAGAAATGAAGTAAAGTAAAGCCCGAGTGTGCC 450

RESULT 23
US-09-949-016-17296/c
; Sequence 17296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17296
; LENGTH: 251682
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17296

Alignment Scores:
Pred. No.: 2.56e+04 Length: 251682
Score: 54.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 40.91% Indels: 0
DB: 3 Gaps: 0

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17296
; LENGTH: 251672
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(251672)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17296

Alignment Scores:
Pred. No.: 2.56e+04 Length: 251672
Score: 54.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 40.91% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-949-016-17296 (1-251672)
Qy 5 GlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 77003 CAGGAGCTCACAGCTGAGATGGGTTTCAGAAATGAAGTAAAGTAAAGCCCGAGTGTGCC 76944

RESULT 24
US-09-949-016-11973/c
; Sequence 11973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11973
; LENGTH: 251682
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(251682)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11973

Alignment Scores:
Pred. No.: 2.56e+04 Length: 251682
Score: 54.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 40.91% Indels: 0
DB: 3 Gaps: 0
```



```
; TYPE: DNA
; ORGANISM: M. musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-978-303-10

Alignment Scores:
Pred. No.: 34.4 Length: 471
Score: 52.00 Matches: 11
Percent Similarity: 68.42% Conservative: 2
Best Local Similarity: 57.89% Mismatches: 4
Query Match: 39.39% Indels: 2
DB: 3 Gaps: 1

US-09-632-036F-6 (1-24) x US-09-978-303-10 (1-471)

QY 8 ThrAlaGluAspGlyThrGlnArgAlaGluLys-----CysSerLysProCysAla 24
Db 30 ACAGCGAGTTCAAAGACCCAGAGACGGAAAGACCTGTCTGCTCAAAGCCATGCTCA 86

RESULT 29
US-09-902-540-6754/c
; Sequence 6754, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6754
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6754

Alignment Scores:
Pred. No.: 88.6 Length: 1062
Score: 52.00 Matches: 9
Percent Similarity: 65.00% Conservative: 4
Best Local Similarity: 45.00% Mismatches: 7
Query Match: 39.39% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-902-540-6754 (1-1062)

QY 3 HisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysPro 22
Db 1035 CACGATCAGCGGTCCACCTCCATCGGGGGCCGACGTCGGGAGGAGTGAATCATCCG 976

RESULT 30
US-08-809-494A-5
; Sequence 5, Application US/08809494A
; Patent No. 5962260
; GENERAL INFORMATION:
; APPLICANT: Sawamura, Tatsuya
; APPLICANT: Maesaki, Tomoo
; TITLE OF INVENTION: Modified Low-Density Lipoprotein
; TITLE OF INVENTION: Receptor
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
; STREET: 261 Madison Avenue
; CITY: New York
; STATE: NY
```

```
; COUNTRY: USA
; ZIP: 10016-2391
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/809,494A
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-321705
; FILING DATE: 30-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-214206
; FILING DATE: 31-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldberg, Jules E
; REGISTRATION NUMBER: 24408
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 986-4090
; TELEFAX: 212 818-9479
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1318 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Lung, placenta
; IMMEDIATE SOURCE:
; LIBRARY: Human lung cDNA
; CLONE: lambdaBLOX-1
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 66..125
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 949..1309
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 127..948
; US-08-809-494A-5
Alignment Scores:
Pred. No.: 114 Length: 1318
Score: 52.00 Matches: 8
Percent Similarity: 59.09% Conservative: 5
Best Local Similarity: 36.36% Mismatches: 9
Query Match: 39.39% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x US-08-809-494A-5 (1-1318)

QY 2 LeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLys 21
Db 493 CTTCAACCACCAAGATCTGAATCTCCAAGAAACACTGAAGAGAGATAGCAAAATTGTTCA 552

QY 22 ProCys 23
Db 553 CCTTGT 558

RESULT 31
US-09-352-302-5
; Sequence 5, Application US/09352302
; Patent No. 6197937
; GENERAL INFORMATION:
```


; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12241
; LENGTH: 141248
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(141248)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12241

Alignment Scores:
Pred. No.: 2.62e+04 141248
Score: 52.00 13
Percent Similarity: 52.94%
Best Local Similarity: 38.24%
Query Match: 39.39%
DB: 3 10 1

US-09-632-036F-6 (1-24) x US-09-949-016-12241 (1-141248)

Qy 1 ProLeuHisAsnGlnGluValThrAla-----Glu 10
Db 23393 CCATCCAGAAACAGAAAGTGACTGCTTATACTGGACGCTGAGCGTGGGCCAACCA 23334
Qy 11 AspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
Db 23333 GACGGACCACAGAAAGCTAAGAAACCCAGCAGGCCAGGACCA 23292

RESULT 38

US-09-949-016-16652/c
; Sequence 16652, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16652
; LENGTH: 143248
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(143248)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16652

Alignment Scores:
Pred. No.: 2.66e+04 143248
Score: 52.00 13
Percent Similarity: 52.94%
Best Local Similarity: 38.24%
Query Match: 39.39%
DB: 3 10 1

US-09-632-036F-6 (1-24) x US-09-949-016-16652 (1-143248)

Qy 1 ProLeuHisAsnGlnGluValThrAla-----Glu 10
Db 73393 CCATCCAGAAACAGAAAGTGACTGCTTATACTGGACGCTGAGCGTGGGCCAACCA 73334
Qy 11 AspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
Db 73333 GACGGACCACAGAAAGCTAAGAAACCCAGCAGGCCAGGACCA 73292

RESULT 39

US-09-385-219A-13/c
; Sequence 13, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiau, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385,219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1763
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-385-219A-13

Alignment Scores:

Pred. No.: 227 Length: 1763
Score: 51.00 Matches: 9
Percent Similarity: 72.22% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 38.64% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-385-219A-13 (1-1763)

Qy 3 HisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1567 CACATCAGAAATAAATACTCGAGATCAGCACCCCAAGGAGTGACATCTGTAGT 1514

RESULT 40

US-09-949-016-137588
; Sequence 137588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137588
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-137588

Alignment Scores:
Pred. No.: 92.1 Length: 601
Score: 50.00 Matches: 10
Percent Similarity: 71.43% Conservative: 0
Best Local Similarity: 71.43% Mismatches: 4
Query Match: 37.88% Indels: 0
DB: 3 Gaps: 0
US-09-632-036F-6 (1-24) x US-09-949-016-137588 (1-601)
Qy 9 AlaGluAspGlyThrGlnArgAlaGluLysCysSerLysPro 22
Db 554 GCTGAGCGAGGAACCCAGGAGCGGGAAGATTGCAGTGACCCG 595

Search completed: December 11, 2005, 01:04:00
Job time : 159.818 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 11, 2005, 00:00:23 ; Search time 470.182 Seconds
(without alignments)
422.103 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLHNQVTAEDGTORAEKCKPCA 24

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-DB=PublishedApplications_NA_Main -QEMT=fastcap -SUFFIX=rnpbm -MINMATCH=0.1
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-TRANS=human40.cdi -LIST=100 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTPMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09632036 @CGN 1.1 1134 orunat_02122005_104143_25924
-NCPU=6 -ICPU=3 -NO_WMAP -LARGQUERY_NEG_SCORES=0 -WAIT_DSFBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-XGAPOP=6 -XGAPEXT=7 -XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA_Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	128	97.0	1260	9	US-10-775-204-1475
3	128	97.0	1320	9	US-10-956-373-25
4	128	97.0	1944	9	US-10-956-373-3
5	128	97.0	2061	9	US-10-956-373-15
6	128	97.0	2132	6	US-10-412-804A-3
7	128	97.0	2149	6	US-10-412-804A-9
8	128	97.0	2164	6	US-10-412-804A-5
9	128	97.0	2164	6	US-10-412-804A-5
10	128	97.0	2164	6	US-10-412-804A-5
11	128	97.0	2164	6	US-10-412-804A-5
12	128	97.0	2164	6	US-10-412-804A-5
13	128	97.0	2164	6	US-10-412-804A-5
14	128	97.0	2164	6	US-10-412-804A-5
15	128	97.0	2164	6	US-10-412-804A-5
16	128	97.0	2164	6	US-10-412-804A-5
17	128	97.0	2164	6	US-10-412-804A-5
18	128	97.0	2164	6	US-10-412-804A-5
19	128	97.0	2164	6	US-10-412-804A-5
20	128	97.0	2164	6	US-10-412-804A-5
21	128	97.0	2164	6	US-10-412-804A-5
22	128	97.0	2164	6	US-10-412-804A-5
23	128	97.0	2164	6	US-10-412-804A-5
24	128	97.0	2164	6	US-10-412-804A-5
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26	128	97.0	2164	6	US-10-412-804A-5
27	128	97.0	2164	6	US-10-412-804A-5
28	128	97.0	2164	6	US-10-412-804A-5
29	128	97.0	2164	6	US-10-412-804A-5
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34	128	97.0	2164	6	US-10-412-804A-5
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36	128	97.0	2164	6	US-10-412-804A-5
37	128	97.0	2164	6	US-10-412-804A-5
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55	114	86.4	3771	3	US-09-811-115-1
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57	114	86.4	3952	3	US-09-870-759-117
58	114	86.4	3955	3	US-09-854-356-10
59	114	86.4	3955	3	US-09-751-708A-117
60	114	86.4	3955	8	US-10-428-817A-113
61	114	86.4	3955	9	US-10-937-758A-94
62	109.5	83.0	3564	9	US-10-794-514A-331
63	108.5	82.2	3504	9	US-10-794-514A-329
64	59	44.7	61791	7	US-10-322-281-645
65	58	43.9	26345	5	US-10-087-192-1705
66	55	41.7	308	8	US-10-425-115-60865
67	55	41.7	541	11	US-10-425-115-103319
68	55	41.7	717	5	US-10-027-632-20298
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74	54	40.9	1245	7	US-10-437-963-70738
75	54	40.9	1263	7	US-10-424-599-33137
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79	53.5	40.5	27423	10	US-11-097-143-3643
80	53	40.2	70	6	US-10-388-360-117
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82 53 40.2 70 8 US-10-714-195-53
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84 53 40.2 70 9 US-10-852-797-324
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86 53 40.2 70 9 US-10-857-715-26
87 53 40.2 578 7 US-10-021-323-9394
88 53 40.2 993 8 US-10-425-115-119394
89 53 40.2 1430 9 US-10-450-763-22332
90 53 40.2 2432 6 US-10-369-493-41562
91 52.5 39.8 468 4 US-09-925-065A-639836
92 52.5 39.8 468 4 US-09-925-065A-639837
93 52.5 39.8 1833 6 US-10-238-075-1563
94 52.5 39.8 2748 6 US-10-238-075-1562
95 52 39.4 456 3 US-09-864-761-1650
96 52 39.4 471 3 US-09-978-303-10
97 52 39.4 471 9 US-10-915-017-10
98 52 39.4 639 8 US-10-765-466-1
99 52 39.4 736 5 US-10-198-846-9641
100 52 39.4 1318 9 US-10-691-532-10

ALIGNMENTS

RESULT 1
US-09-878-134-68
; Sequence 68, Application US/09878134
; Publication No. US20020086303A1
; GENERAL INFORMATION:
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: King, Gordon E.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.532
; CURRENT APPLICATION NUMBER: US/09/878,134
; CURRENT FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: Corixa Invention Disclosure Database
; SEQ ID NO 68
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-878-134-68
Alignment Scores:
Pred. No.: 1,59e-12 Length: 471
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-878-134-68 (1-471)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 65 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAAGTGCAGC 124
Qy 21 LysProCysAla 24
Db 125 AAGCCCTGTGCC 136

RESULT 2
US-10-775-204-1475
; Sequence 1475, Application US/10775204
; Publication No. US20050186664A1
; GENERAL INFORMATION:
; APPLICANT: Rosen, Craig A.
; APPLICANT: Haseltine, William A.
; APPLICANT: Balance, David J.
; APPLICANT: Turner, Andrew J.
; TITLE OF INVENTION: Albumin Fusion Proteins

; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/10/775,204
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1475
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-775-204-1475
Alignment Scores:
Pred. No.: 4,88e-12 Length: 1260
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 9 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-775-204-1475 (1-1260)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAAGTGCAGC 1005

Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 3

US-10-956-373-25
; Sequence 25, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ErbB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 25
; LENGTH: 1320

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-373-25

Alignment Scores:
Pred. No.: 5,14e-12 Length: 1320
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 9 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-956-373-25 (1-1320)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAAACACACGGTGTGAGAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 4

US-10-956-373-3

; Sequence 3, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:

; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 3
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-373-3

Alignment Scores:

Pred. No.: 8e-12 Length: 1944
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 9 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-956-373-3 (1-1944)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAAACACACGGTGTGAGAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 5

US-10-956-373-15

; Sequence 15, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen

; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: METHODS USING SAME
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-373-15

Alignment Scores:

Pred. No.: 8.55e-12 Length: 2061
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 9 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-956-373-15 (1-2061)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAAACACACGGTGTGAGAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 6

US-10-412-804A-3
; Sequence 3, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:

; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; FILE REFERENCE: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2132
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (78)..(2132)
US-10-412-804A-3

Alignment Scores:

Pred. No.: 8.89e-12 Length: 2132
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-412-804A-3 (1-2132)

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QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1023 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAAGTGCAGC 1082

QY 21 LysProCysAla 24
Db 1083 AAGCCCTGTGCC 1094

RESULT 7
US-10-412-804A-9
; Sequence 9, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Tatatewicz, Suzanna
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2145)
US-10-412-804A-9

Alignment Scores:
Pred. No.: 8,97e-12 Length: 2149
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
Gaps: 0

US-09-632-036F-6 (1-24) x US-10-412-804A-9 (1-2149)
; Sequence 5, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Tatatewicz, Suzanna
; APPLICANT: Jing, Shuguan
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2164
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2160)
US-10-412-804A-5

Alignment Scores:
Pred. No.: 9,79e-12 Length: 2320
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
Gaps: 0

US-09-632-036F-6 (1-24) x US-10-956-373-1 (1-2320)
; Sequence 1, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Beiman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinmeret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ErbB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-373-1

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAAGTGCAGC 1155

QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 10
US-10-956-373-13
; Sequence 13, Application US/10956373
; Publication No. US20050123538A1
; GENERAL INFORMATION:
; APPLICANT: Shemesh, Ronen
```

```
; APPLICANT: Oren, Anat
; APPLICANT: Rotman, Galit
; APPLICANT: Sela-Tavor, Osnat
; APPLICANT: Walach, Shira
; APPLICANT: Sameah-Greenwald, Shirley
; APPLICANT: Belman, Merav
; APPLICANT: Eshel, Dani
; APPLICANT: Savitsky, Kinneret
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL ERBB-2 POLYPEPTIDES AND KITS AND
; FILE REFERENCE: 28399
; CURRENT APPLICATION NUMBER: US/10/956,373
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 2437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-373-13
Alignment Scores:
Pred. No.: 1,04e-11 Length: 2437
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 9 Gaps: 0
US-09-632-036F-6 (1-24) x US-10-956-373-13 (1-2437)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACACGCGTGTGAGAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167
RESULT 11
US-10-207-498-5
; Sequence 5, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizabeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; FILE REFERENCE: 30448.103-US-U1
; CURRENT APPLICATION NUMBER: US/10/207,498
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3765
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-207-498-5
Alignment Scores:
Pred. No.: 1,7e-11 Length: 3765
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0
```

```
US-09-632-036F-6 (1-24) x US-10-207-498-5 (1-3765)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACACGCGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 12
US-09-811-123-8
; Sequence 8, Application US/09811123
; Patent No. US20020001587A1
; GENERAL INFORMATION:
; APPLICANT: Sharon Erickson
; APPLICANT: Ralph Schwall
; APPLICANT: Mark Sliwkowski
; TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-ERBB
; FILE REFERENCE: GENENT.073A2
; CURRENT APPLICATION NUMBER: US/09/811,123
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/238,327
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: 09/602,530
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-123-8
Alignment Scores:
Pred. No.: 1,7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0
US-09-632-036F-6 (1-24) x US-09-811-123-8 (1-3768)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACACGCGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017
RESULT 13
US-09-811-115-2
; Sequence 2, Application US/09811115
; Patent No. US20020035736A1
; GENERAL INFORMATION:
; APPLICANT: Erickson, Sharon
; APPLICANT: Schwall, Ralph
; APPLICANT: King, Kathleen
; TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
; FILE REFERENCE: GENENT.034A
; CURRENT APPLICATION NUMBER: US/09/811,115
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/189,844
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3768
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
US-09-811-115-2

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-811-115-2 (1-3768)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCAACCAACAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 14
US-09-765-973-1
; Sequence 1, Application US/09765973
; Publication No. US20020039573A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR PREVENTION AND
; FILE OF INVENTION: TREATMENT OF HER-2/neu ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.496
; CURRENT FILING DATE: 2001-01-19
; CURRENT APPLICATION NUMBER: US/09/765,973
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-765-973-1

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-765-973-1 (1-3768)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCAACCAACAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 15
US-09-854-356-9
; Sequence 9, Application US/09854356
; Patent No. US2002017567A1
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Gheysen, Dirk
; APPLICANT: Corixa Corporation
; APPLICANT: SmithKline Beecham Biologicals S. A.
; TITLE OF INVENTION: HER-2/neu Fusion Proteins
; FILE REFERENCE: 014058-009810PC

; CURRENT APPLICATION NUMBER: US/09/854,356
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: US 09/493,480
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,976
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3768)
; OTHER INFORMATION: human HER-2/neu protein
; NAME/KEY: misc_feature
; LOCATION: (1)..(1959)
; OTHER INFORMATION: extracellular domain (ECD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2026)..(3765)
; OTHER INFORMATION: intracellular domain (ICD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3765)
; OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
; NAME/KEY: misc_feature
; LOCATION: (2968)..(3144)
; OTHER INFORMATION: preferred portion of the phosphorylation domain
; OTHER INFORMATION: (delta PD) of human HER-2/neu
US-09-854-356-9

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-854-356-9 (1-3768)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCTGCAACCAACAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 16
US-09-930-125-1
; Sequence 1, Application US/09930125
; Publication No. US20020193329A1
; GENERAL INFORMATION:
; APPLICANT: Hand-Zimmerman, Susan
; APPLICANT: Cheever, Martin A.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Vedvick, Thomas S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
; OF HER-2/NEU-ASSOCIATED MALIGNANCIES
; FILE REFERENCE: 210121.544
; CURRENT APPLICATION NUMBER: US/09/930,125
; CURRENT FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-09-930-125-1

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-930-125-1 (1-3768)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 17
US-09-984-092-3
; Sequence 3, Application US/09984092
; Publication No. US20040037840A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL THERAPEUTIC VACCINE FORMULATIONS
; FILE REFERENCE: P1011PC00
; CURRENT APPLICATION NUMBER: US/09/984,092
; CURRENT FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3768)
US-09-984-092-3

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x US-09-984-092-3 (1-3768)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 18
US-10-313-644-1
; Sequence 1, Application US/10313644
; Publication No. US20030157119A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; APPLICANT: Hand-Zimmerman, Susan
; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
; FILE REFERENCE: 210121.483C3
; CURRENT APPLICATION NUMBER: US/10/313,644
```

```
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(3765)
US-10-313-644-1

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-313-644-1 (1-3768)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 19
US-10-280-576-3
; Sequence 3, Application US/10280576
; Publication No. US20040044405A1
; GENERAL INFORMATION:
; APPLICANT: Wolff, Matthew R.
; TITLE OF INVENTION: VASCULAR STENT OR GRAFT COATED OR IMPREGNATED WITH PROTEIN
; FILE REFERENCE: 09820.189
; CURRENT APPLICATION NUMBER: US/10/280,576
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/343,732
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3768
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-280-576-3

Alignment Scores:
Pred. No.: 1.7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-280-576-3 (1-3768)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACCAACCAAGAGGTGCACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1005
Qy 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 20
US-10-441-779C-3
; Sequence 3, Application US/10441779C
; Publication No. US20040141958A1
; GENERAL INFORMATION:
```

```
/ APPLICANT: Steinaa, Lucilla
/ APPLICANT: Mouritsen, Soren
/ APPLICANT: Gautam, Anand
/ APPLICANT: Haaning, Jesper
/ APPLICANT: Dalum, Iben
/ APPLICANT: Birk, Peter
/ APPLICANT: Leach, Dana
/ APPLICANT: Karlsson, Klaus
/ TITLE OF INVENTION: NOVEL METHODS FOR THERAPEUTIC VACCINATION
/ FILE REFERENCE: 4614-0116P
/ CURRENT APPLICATION NUMBER: US/10/441,779C
/ CURRENT FILING DATE: 2003-05-19
/ PRIOR APPLICATION NUMBER: 09/413,186
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: 60/105,011
/ PRIOR FILING DATE: 1998-10-20
/ PRIOR APPLICATION NUMBER: PA 1998 01361
/ PRIOR FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 41
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 3768
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1)..(3768)
/ OTHER INFORMATION:
US-10-441-779C-3

Alignment Scores:
Pred. No.: 1-7e-11 Length: 3768
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: Gaps: 0

US-09-632-036F-6 (1-24) x US-10-441-779C-3 (1-3768)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACAAACAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 21
US-10-384-339C-52
/ Sequence 52, Application US/10384339C
/ Publication No. US20040175703A1
/ GENERAL INFORMATION:
/ APPLICANT: Kreutzer, Roland
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
/ FILE REFERENCE: 20200/2002
/ CURRENT APPLICATION NUMBER: US/10/384,339C
/ CURRENT FILING DATE: 2003-03-07
/ PRIOR APPLICATION NUMBER: PCT/EP02/00152
/ PRIOR FILING DATE: 2002-01-09
/ PRIOR APPLICATION NUMBER: DE 10100586.5
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: DE 10155280.7
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: DE 10158411.3
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: DE 10160151.4
/ PRIOR FILING DATE: 2001-12-07
/ NUMBER OF SEQ ID NOS: 173
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 3768

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 946 CCCCTGCACAAACAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAAGTGCAGC 1005

QY 21 LysProCysAla 24
Db 1006 AAGCCCTGTGCC 1017

RESULT 21
US-10-384-339C-52
/ Sequence 52, Application US/10384339C
/ Publication No. US20040175703A1
/ GENERAL INFORMATION:
/ APPLICANT: Kreutzer, Roland
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
/ FILE REFERENCE: 20200/2002
/ CURRENT APPLICATION NUMBER: US/10/384,339C
/ CURRENT FILING DATE: 2003-03-07
/ PRIOR APPLICATION NUMBER: PCT/EP02/00152
/ PRIOR FILING DATE: 2002-01-09
/ PRIOR APPLICATION NUMBER: DE 10100586.5
/ PRIOR FILING DATE: 2001-01-09
/ PRIOR APPLICATION NUMBER: DE 10155280.7
/ PRIOR FILING DATE: 2001-10-26
/ PRIOR APPLICATION NUMBER: DE 10158411.3
/ PRIOR FILING DATE: 2001-11-29
/ PRIOR APPLICATION NUMBER: DE 10160151.4
/ PRIOR FILING DATE: 2001-12-07
/ NUMBER OF SEQ ID NOS: 173
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 52
/ LENGTH: 3768

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1120 CCCCTGCACAAACAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAAGTGCAGC 1179

QY 21 LysProCysAla 24
Db 1180 AAGCCCTGTGCC 1191

RESULT 23
US-10-146-473-32
/ Sequence 32, Application US/10146473
/ Publication No. US2003010888A1
/ GENERAL INFORMATION:
/ APPLICANT: Scanlan, Matthew
/ APPLICANT: Gout, Ivan
/ APPLICANT: Stockert, Elisabeth
/ APPLICANT: Gure, Ali
```

```
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: Breast Cancer Antigens
; FILE REFERENCE: L00461/70130(JRV)
; CURRENT APPLICATION NUMBER: US/10/146.473
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/291,150
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-473-32

Alignment Scores:
Pred. No.: 2,07e-11 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 5 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-146-473-32 (1-4473)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 1120 CCCTGCAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAGTGCAGC 1179

Qy 21 LysProCysAla 24
|||
Db 1180 AAGCCCTGTGCC 1191

RESULT 24
US-10-207-655-44
; Sequence 44, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207.655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-207-655-44

Alignment Scores:
Pred. No.: 2,07e-11 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 5 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-207-655-44 (1-4473)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 1120 CCCTGCAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAGTGCAGC 1179

Qy 21 LysProCysAla 24
|||
Db 1180 AAGCCCTGTGCC 1191

RESULT 25
US-10-101-510-81
; Sequence 81, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101.510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-81

Alignment Scores:
Pred. No.: 2,07e-11 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-101-510-81 (1-4473)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 1120 CCCTGCAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAGTGCAGC 1179

Qy 21 LysProCysAla 24
|||
Db 1180 AAGCCCTGTGCC 1191

RESULT 26
US-10-762-128-5
; Sequence 5, Application US/10762128
; Publication No. US20040219161A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Disis, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409C1
; CURRENT APPLICATION NUMBER: US/10/762.128
; CURRENT FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 09/441,411
; PRIOR FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-762-128-5

Alignment Scores:
Pred. No.: 2,07e-11 Length: 4473
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 8 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-762-128-5 (1-4473)
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
|||
Db 1120 CCCTGCAACCAAGAGGTGACAGCAGAGGATGGAAACACACAGCGGTGTGAGAGTGCAGC 1179
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QY      21 LysProCysAla 24
Db      1180 AAGCCCTGTGCC 1191

RESULT 27
US-10-723-860-8
; Sequence 8, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 4473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-860-8

Alignment Scores:
Pred. No.:      2,07e-11      Length:      4473
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches: 1
Query Match:    96.97%      Indels:      0
DB:             8          Gaps:      0

US-09-632-036F-6 (1-24) x US-10-723-860-8 (1-4473)

QY      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1120 CCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1179

QY      21 LysProCysAla 24
Db      1180 AAGCCCTGTGCC 1191

RESULT 28
US-09-877-177-11
; Sequence 11, Application US/09877177
; Publication No. US20020192652A1
; GENERAL INFORMATION:
; APPLICANT: Peter V. Danenberg et al.
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-New Gene Expression
; FILE REFERENCE: 11220/120
; CURRENT APPLICATION NUMBER: US/09/877,177
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-877-177-11

Alignment Scores:
Pred. No.:      2.1e-11      Length:      4530
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches: 1
Query Match:    96.97%      Indels:      0
DB:             3          Gaps:      0
```

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US-09-632-036F-6 (1-24) x US-09-877-177-11 (1-4530)

QY      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1096 CCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155

QY      21 LysProCysAla 24
Db      1156 AAGCCCTGTGCC 1167

RESULT 29
US-10-177-293-125
; Sequence 125, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-125

Alignment Scores:
Pred. No.:      2.1e-11      Length:      4530
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches: 1
Query Match:    96.97%      Indels:      0
DB:             6          Gaps:      0

US-09-632-036F-6 (1-24) x US-10-177-293-125 (1-4530)

QY      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1096 CCCTGCACAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAAGTGCAGC 1155

QY      21 LysProCysAla 24
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Db      1156 AAGCCCTGTGCC 1167
|||||
RESULT 30
US-10-007-926A-119
; Sequence 119, Application US/10007926A
; Publication No. US20030143539A1
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 119
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: v-erb-b2 avian erythroblastic leukemia viral
; OTHER INFORMATION: oncogene homolog 2 (neuro/glioblastoma derived
; OTHER INFORMATION: oncogene homolog) (ERBB2) gene.
US-10-007-926A-119
Alignment Scores:
Pred. No.:      2,1e-11      Length:      4530
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches:  1
Query Match:    96.97%      Indels:      0
DB:             6          Gaps:          0

US-09-632-036F-6 (1-24) x US-10-007-926A-119 (1-4530)
Qy      1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1096 CCCTGACACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1155
Qy      21 LysProCysAla 24
Db      1156 AAGCCCTGTGCC 1167
|||||
RESULT 31
US-10-338-730-1
; Sequence 1, Application US/10338730
; Publication No. US20030147905A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS
; FILE REFERENCE: 5017C
; CURRENT APPLICATION NUMBER: US/10/338,730
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US 09/527,487
; PRIOR FILING DATE: 2002-03-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (151)..(3915)

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; OTHER INFORMATION:
US-10-338-730-1
Alignment Scores:
Pred. No.:      2,1e-11      Length:      4530
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches:  1
Query Match:    96.97%      Indels:      0
DB:             6          Gaps:          0

US-09-632-036F-6 (1-24) x US-10-338-730-1 (1-4530)
Qy      1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1096 CCCTGACACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1155
Qy      21 LysProCysAla 24
Db      1156 AAGCCCTGTGCC 1167
|||||
RESULT 32
US-10-101-510-124
; Sequence 124, Application US/10101510
; Publication No. US20030148295A1
; GENERAL INFORMATION:
; APPLICANT: WAN, JACKSON
; APPLICANT: WANG, YIXIN
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE
; FILE REFERENCE: 15117.0012
; CURRENT APPLICATION NUMBER: US/10/101,510
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/276,947
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 805
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-101-510-124
Alignment Scores:
Pred. No.:      2,1e-11      Length:      4530
Score:          128.00      Matches:      23
Percent Similarity: 95.83%      Conservative: 0
Best Local Similarity: 95.83%      Mismatches:  1
Query Match:    96.97%      Indels:      0
DB:             6          Gaps:          0

US-09-632-036F-6 (1-24) x US-10-101-510-124 (1-4530)
Qy      1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      1096 CCCTGACACCAACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCAGC 1155
Qy      21 LysProCysAla 24
Db      1156 AAGCCCTGTGCC 1167
|||||
RESULT 33
US-10-116-275-131
; Sequence 131, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors

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; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-116-275-131

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-116-275-131 (1-4530)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAACACACGCGGTGTGAGAAGTGCAGC 1155

QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 34
US-10-426-836-11
; Sequence 11, Application US/10426836
; Publication No. US20030211530A1
; GENERAL INFORMATION:
; APPLICANT: K. Danenberg
; TITLE OF INVENTION: Method of determining Epidermal Growth
; TITLE OF INVENTION: Factor Receptor and HER2-Neu Gene Expression
; FILE REFERENCE: 11220/169
; CURRENT APPLICATION NUMBER: US/10/426,836
; CURRENT FILING DATE: 2003-05-01
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-426-836-11

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-426-836-11 (1-4530)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAACACACGCGGTGTGAGAAGTGCAGC 1155

QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 35
US-10-272-437A-27
; Sequence 27, Application US/10272437A
; Publication No. US20030216309A1
; GENERAL INFORMATION:
; APPLICANT: Krag, David N.
```

```
; APPLICANT: Pero, Stephanie C.
; APPLICANT: Oligino, Lyn
; TITLE OF INVENTION: BINDING PEPTIDES SPECIFIC FOR THE EXTRACELLULAR DOMAIN OF ERBB2
; TITLE OF INVENTION: USES THEREFOR
; FILE REFERENCE: V00139.70056.US
; CURRENT APPLICATION NUMBER: US/10/272,437A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/329,183
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-437A-27

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-272-437A-27 (1-4530)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCTGACAAACCAAGAGGTGACAGCAGAGGATGGAACACACGCGGTGTGAGAAGTGCAGC 1155

QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 36
US-10-117-937-595
; Sequence 595, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPI TOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 595
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-117-937-595

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-117-937-595 (1-4530)
```

```
Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 37
US-10-392-113-45
; Sequence 45, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; TITLE OF INVENTION: OF CANCER CELLS
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392.113
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-45

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-392-113-45 (1-4530)
Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 38
US-10-159-563-208
; Sequence 208, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
```

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; SEQ ID NO 208
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-208

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-159-563-208 (1-4530)
Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 39
US-10-435-696-10
; Sequence 10, Application US/10435696
; Publication No. US20040018525A1
; GENERAL INFORMATION:
; APPLICANT: Wirtz, Ralph
; APPLICANT: Munnes, Marc
; APPLICANT: Kallabis, Harald
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE PREDICTION, DIAGNOSIS, PROGNOSIS
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
; FILE REFERENCE: Lea 36 108
; CURRENT APPLICATION NUMBER: US/10/435,696
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: EP03003112.4
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: EP02010291.9
; PRIOR FILING DATE: 2002-05-21
; NUMBER OF SEQ ID NOS: 314
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-435-696-10

Alignment Scores:
Pred. No.: 2,1e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-435-696-10 (1-4530)
Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAAGTGCAGC 1155
Qy 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 40
US-10-734-564-59
; Sequence 59, Application US/10734564
; Publication No. US20040157278A1
; GENERAL INFORMATION:
; APPLICANT: Christopher C Burgess et al
```

; TITLE OF INVENTION: Detection Methods Using TIMP1

; FILE REFERENCE: 1657/2012

; CURRENT APPLICATION NUMBER: US/10/734,564

; CURRENT FILING DATE: 2003-12-12

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 59

; LENGTH: 4530

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-734-564-59

Alignment Scores:

Pred. No.:	2,1e-11	Length:	4530
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	7	Gaps:	0

US-09-632-036F-6 (1-24) x US-10-734-564-59 (1-4530)

Qy	1	ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer	20
Db	1096	CCCCCTGCACCAACCAAGAGGTGACAGAGGTGAACACAGCGGTGTGAGAAAGTGAGC	1155
Qy	21	LysProCysAla	24
Db	1156	AAGCCCTGTGCC	1167

Search completed: December 11, 2005, 03:11:47

481 182 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 11, 2005, 01:00:20 ; Search time 143.455 Seconds
(without alignments)
62.546 Million cell updates/sec

Title: US-09-632-036F-6

Perfect score: 132

Sequence: 1 PLNNQVTAEDGTQRAEKSCKPCA 24

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-DB=Published Applications NA_New -QFMT=fastcap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=bloms62
-TRANS=human40.cdi -LIST=100 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=40 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09632036@cgn.1.1.227@runat_02122005_104143_25959
-NCPU=6 -ICPU=1 -NO MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	97.0	4530	6	US-10-770-726-18
2	128	97.0	149419	7	US-11-112-908-49
3	128	97.0	157224	7	US-11-112-908-51
4	128	97.0	161726	7	US-11-112-908-48
5	128	97.0	161726	7	US-11-112-908-52
C 6	57	43.2	690	6	US-10-467-657-3887
7	54	40.9	184868	7	US-11-121-086-88
C 8	51.5	39.0	1302	6	US-10-467-657-345
					Sequence 18, Appl
					Sequence 49, Appl
					Sequence 51, Appl
					Sequence 48, Appl
					Sequence 52, Appl
					Sequence 3887, Ap
					Sequence 88, Appl
					Sequence 345, App

C 9	51	38.6	1763	6	US-10-632-150-13	Sequence 13, Appl
C 10	51	38.6	1763	7	US-11-073-457-13	Sequence 13, Appl
C 11	51	38.6	1794	7	US-11-074-176-257	Sequence 257, App
C 12	50.5	38.3	780	9	US-11-082-389-249	Sequence 249, App
C 13	49.5	37.5	2766	6	US-10-750-185-55939	Sequence 55939, A
C 14	49.5	37.5	178877	7	US-11-121-086-17	Sequence 17, Appl
C 15	49	37.1	600	6	US-10-750-185-1366	Sequence 1366, Ap
C 16	49	37.1	168516	7	US-11-121-086-3	Sequence 3, Appl
C 17	49	37.1	190882	7	US-11-121-086-69	Sequence 69, Appl
C 18	48	36.4	1430	6	US-10-750-185-61160	Sequence 61160, A
C 19	48	36.4	1795	6	US-10-750-185-41622	Sequence 41622, A
C 20	48	36.4	124972	7	US-11-121-086-100	Sequence 100, App
C 21	48	36.4	134174	7	US-11-121-086-99	Sequence 99, Appl
C 22	47	35.6	1634	6	US-10-750-185-40234	Sequence 40234, A
C 23	47	35.6	1082144	7	US-11-117-187-211	Sequence 211, App
C 24	46.5	35.2	1219	6	US-10-750-185-54567	Sequence 54567, A
C 25	46	34.8	1490	6	US-10-750-185-47299	Sequence 47299, A
C 26	46	34.8	1670	6	US-10-614-599-2	Sequence 2, Appl
C 27	46	34.8	2151	7	US-11-147-047-26	Sequence 26, Appl
C 28	46	34.8	2254	6	US-10-750-185-56790	Sequence 56790, A
C 29	46	34.8	2377	6	US-10-750-185-62314	Sequence 62314, A
C 30	46	34.8	2658	6	US-10-131-826A-511	Sequence 511, App
C 31	46	34.8	64415	7	US-11-117-187-185	Sequence 185, App
C 32	46	34.8	150314	7	US-11-112-908-24	Sequence 24, Appl
C 33	46	34.8	163317	7	US-11-117-187-212	Sequence 212, App
C 34	46	34.8	189539	7	US-11-121-086-16	Sequence 16, Appl
C 35	46	34.8	218821	7	US-11-121-086-31	Sequence 31, Appl
C 36	45.5	34.5	153142	7	US-11-121-086-27	Sequence 27, Appl
C 37	45	34.1	1649	6	US-10-750-185-24998	Sequence 24998, A
C 38	45	34.1	1713	6	US-10-750-185-56624	Sequence 56624, A
C 39	45	34.1	2838	6	US-10-750-185-46440	Sequence 46440, A
C 40	45	34.1	92584	7	US-11-117-187-194	Sequence 194, App
C 41	45	34.1	150314	7	US-11-112-908-24	Sequence 24, Appl
C 42	45	34.1	180654	7	US-11-121-086-58	Sequence 58, Appl
C 43	44.5	33.7	816	6	US-10-750-185-60284	Sequence 60284, A
C 44	44.5	33.7	1609	6	US-10-750-185-55040	Sequence 55040, A
C 45	44.5	33.7	3334	6	US-10-750-185-34055	Sequence 34055, A
C 46	44.5	33.7	167891	7	US-11-121-086-14	Sequence 14, Appl
C 47	44	33.3	1056	6	US-10-467-657-2437	Sequence 2437, Ap
C 48	44	33.3	1286	6	US-10-750-185-25304	Sequence 25304, A
C 49	44	33.3	1321	6	US-10-750-185-49780	Sequence 49780, A
C 50	44	33.3	1356	6	US-10-750-185-53605	Sequence 53605, A
C 51	44	33.3	2819	8	US-11-112-944-13	Sequence 13, Appl
C 52	44	33.3	3432	6	US-10-467-657-1819	Sequence 1819, Ap
C 53	44	33.3	3602	6	US-10-750-185-28825	Sequence 28825, A
C 54	44	33.3	79122	7	US-11-117-187-200	Sequence 200, App
C 55	44	33.3	148220	7	US-11-121-086-90	Sequence 90, Appl
C 56	44	33.3	150481	7	US-11-112-908-37	Sequence 37, Appl
C 57	44	33.3	179777	7	US-11-121-086-106	Sequence 106, App
C 58	44	33.3	179892	7	US-11-112-908-39	Sequence 39, Appl
C 59	44	33.3	197056	7	US-11-121-086-107	Sequence 107, App
C 60	43.5	33.0	600	6	US-10-750-185-21076	Sequence 21076, A
C 61	43.5	33.0	1124	6	US-10-750-185-41659	Sequence 41659, A
C 62	43.5	33.0	1295	6	US-10-131-826A-335	Sequence 335, App
C 63	43.5	33.0	185393	7	US-11-121-086-101	Sequence 101, App
C 64	43	32.6	600	6	US-10-750-185-21492	Sequence 21492, A
C 65	43	32.6	600	6	US-10-750-185-41507	Sequence 41507, A
C 66	43	32.6	670	6	US-10-750-185-61723	Sequence 61723, A
C 67	43	32.6	1340	6	US-10-750-185-57537	Sequence 57537, A
C 68	43	32.6	1377	6	US-10-742-634-6	Sequence 6, Appl
C 69	43	32.6	1561	6	US-10-750-185-48239	Sequence 48239, A
C 70	43	32.6	1580	6	US-10-750-185-32368	Sequence 32368, A
C 71	43	32.6	1612	6	US-10-750-185-31631	Sequence 31631, A
C 72	43	32.6	1808	6	US-10-750-185-40283	Sequence 40283, A
C 73	43	32.6	1869	6	US-10-750-185-48903	Sequence 48903, A
C 74	43	32.6	2326	6	US-10-750-185-38395	Sequence 38395, A
C 75	43	32.6	2721	6	US-10-750-185-52450	Sequence 52450, A
C 76	43	32.6	3591	6	US-10-667-295-99	Sequence 99, Appl
C 77	43	32.6	5260	6	US-10-750-185-25097	Sequence 25097, A
C 78	43	32.6	5796	6	US-10-821-234-62	Sequence 62, Appl
C 79	43	32.6	6087	7	US-11-000-463-485	Sequence 485, App
C 80	43	32.6	6116	7	US-11-000-463-13	Sequence 13, Appl
C 81	43	32.6	154548	7	US-11-121-086-33	Sequence 33, Appl

Sequence 43, Appl
Sequence 20, Appl
Sequence 50, Appl
Sequence 24, Appl
Sequence 36, Appl
Sequence 50, Appl
Sequence 11, Appl
Sequence 2939, A
Sequence 32500, A
Sequence 7, Appl
Sequence 96, Appl
Sequence 51, Appl
Sequence 77, Appl
Sequence 401, App
Sequence 923, App
Sequence 230, App
Sequence 28491, A
Sequence 31610, A
Sequence 37352, A

ALIGNMENTS

RESULT 1
US-10-770-726-18
; Sequence 18, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-18

Alignment Scores:
Pred. No.: 1.68e-11 Length: 4530
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-770-726-18 (1-4530)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 1096 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGC 1155

QY 21 LysProCysAla 24
Db 1156 AAGCCCTGTGCC 1167

RESULT 2
US-11-112-908-49
; Sequence 49, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 149419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-49

Alignment Scores:
Pred. No.: 1.26e-09 Length: 149419
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-112-908-49 (1-149419)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 6108 CCCCTGCACAAACCAAGAGGTGACAGCAGAGGATGGAACACAGCGGTGTGAGAAGTGCAGC 6167

QY 21 LysProCysAla 24
Db 6168 AAGCCCTGTGCC 6179

RESULT 3
US-11-112-908-51
; Sequence 51, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT FILING DATE: 2005-04-22
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 157224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-51

Alignment Scores:
Pred. No.: 1.34e-09 Length: 157224
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservatives: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-112-908-51 (1-157224)
QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

Db 142585 CCCTGCACCAACCAAGAGGTGACACGAGGATGGAAACACAGCGGTGTGAGAAAGTGCAGC 142644

Qy 21 LysProCysAla 24
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Db 142645 AAGCCCTGTGCC 142656

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US-11-112-908-48
; Sequence 48, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 48
; LENGTH: 161726
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-112-908-48

Alignment Scores:

Pred. No.:	1.39e-09	Length:	161726
Score:	128.00	Matches:	23
Percent Similarity:	95.83%	Conservative:	0
Best Local Similarity:	95.83%	Mismatches:	1
Query Match:	96.97%	Indels:	0
DB:	7	Gaps:	0

US-09-632-036F-6 (1-24) x US-11-112-908-48 (1-161726)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAaspGlyThrGlnArgAlaGluLysCysSer 20
|||||

Db 56390 CCCTGCACCAACCAAGAGGTGACACGAGGATGGAAACACAGCGGTGTGAGAAAGTGCAGC 56449

Qy 21 LysProCysAla 24
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Db 56450 AAGCCCTGTGCC 56461

RESULT 5

US-11-112-908-52
; Sequence 52, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52

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; LENGTH: 161726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-52

Alignment Scores:
Pred. No.: 1.39e-09 Length: 161726
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-112-908-52 (1-161726)

Qy 1 ProLeuHisAsnGlnCluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 56390 CCCTGCAACCAAGAGGTGACAGCAGAGGATGGAAACACACACGCGGTGTGAGAAAGTGCAGC 56449

Qy 21 LysProCysAla 24
Db 56450 AAGCCCTGTGCC 56461

RESULT 6
US-10-467-657-3887/c
; Sequence 3887, Application US10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3887
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3887

Alignment Scores:
Pred. No.: 3.62 Length: 690
Score: 57.00 Matches: 11
Percent Similarity: 63.64% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 43.18% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-467-657-3887 (1-690)

Qy 3 HisAsnGlnCluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysPro 22
Db 600 AATAACCAACGACCGCGATGCCGAACCAAGCGGCAGTCAGCGCGCCCAAAAGATAAAGCCAAA 541

Qy 23 CysAla 24
Db 540 TGTGCG 535

RESULT 7
US-11-121-086-88
; Sequence 88, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: FOULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

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; LENGTH: 161726
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-52

Alignment Scores:
Pred. No.: 1.39e-09 Length: 161726
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-112-908-52 (1-161726)

Qy 1 ProLeuHisAsnGlnClnValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 56390 CCCTTCACAACCAAGAGGTGACAGAGAGGTGAACACAGCGGTGTGAGAAAGTGCAGC 56
Qy 21 LysProCysAla 24
Db 56450 AAGCCCTGTGCC 56461

RESULT 6
US-10-467-657-3887/c
; Sequence 3887, Application US10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3887
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3887

Alignment Scores:
Pred. No.: 3.62 Length: 690
Score: 57.00 Matches: 11
Percent Similarity: 63.64% Conservative: 3
Best Local Similarity: 50.00% Mismatches: 8
Query Match: 43.18% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-467-657-3887 (1-690)

Qy 3 HisAsnGlnClnValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysPro 20
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Qy 23 CysAla 24
Db 540 TGTGCG 535

RESULT 7
US-11-121-086-88
; Sequence 88, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

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/ FILE REFERENCE: 09138.6000-00000
/ CURRENT APPLICATION NUMBER: US/11/121,086
/ CURRENT FILING DATE: 2005-05-04
/ PRIOR APPLICATION NUMBER: 60/567,570
/ PRIOR FILING DATE: 2004-05-04
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: Patent in version 3.3
/ SEQ ID NO 88
/ LENGTH: 184868
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-11-121-086-88
```

```
Alignment Scores:
Pred. No.: 1,2e+04 Length: 184868
Score: 54.00 Matches: 11
Percent Similarity: 65.00% Conservative: 2
Best Local Similarity: 55.00% Mismatches: 7
Query Match: 40.91% Indels: 0
DB: 7 Gaps: 0
```

US-09-632-036F-6 (1-24) x US-11-121-086-88 (1-184868)

```
Qy 5 GlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
Db 1665 CAGGAGCTCACAGCTGAGATGGGGTTTCAGAAATGAAGTAAGTAAAGCCAGCTGTGCC 1724
```

RESULT 8

```
US-10-467-657-345/c
/ Sequence 345, Application US/10467657
/ Publication No. US20050260581A1
```

GENERAL INFORMATION:

```
/ APPLICANT: CHIRON SpA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONGOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
```

```
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
```

```
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 345
/ LENGTH: 1302
/ TYPE: DNA
/ ORGANISM: Neisseria gonorrhoeae
```

US-10-467-657-345

```
Alignment Scores:
Pred. No.: 71.7 Length: 1302
Score: 51.50 Matches: 10
Percent Similarity: 57.69% Conservative: 5
Best Local Similarity: 38.46% Mismatches: 8
Query Match: 39.02% Indels: 3
DB: 6 Gaps: 1
```

US-09-632-036F-6 (1-24) x US-10-467-657-345 (1-1302)

```
Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArg-----AlaGlu 17
Db 816 CCCATCCACATCAGCGTATCGCGCTGATTGACGGGAATCAGCGGAATCTCGGCCGGAAG 757
```

Qy 18 LysCysSerLysProCys 23

Db 756 CGACCTCTCTCGACCGTGC 739

RESULT 9

```
US-10-632-150-13/c
/ Sequence 13, Application US/10632150
/ Publication No. US20050251871A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Chiau, D.
/ APPLICANT: Pagano, M.
/ APPLICANT: Latres, E.
/ TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
/ FILE REFERENCE: 5914-081
```

```
/ CURRENT APPLICATION NUMBER: US/10/632,150
/ CURRENT FILING DATE: 2003-07-30
/ PRIOR APPLICATION NUMBER: US/09/385,219
```

```
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/098,355
```

```
/ PRIOR FILING DATE: 1998-08-28
/ PRIOR APPLICATION NUMBER: 60/118,568
```

```
/ PRIOR FILING DATE: 1999-02-03
/ PRIOR APPLICATION NUMBER: 60/124,449
```

```
/ PRIOR FILING DATE: 1999-03-15
/ NUMBER OF SEQ ID NOS: 90
```

```
/ SOFTWARE: Patent in Ver. 2.0
/ SEQ ID NO 13
```

```
/ LENGTH: 1763
/ TYPE: DNA
/ ORGANISM: Homo sapiens
```

US-10-632-150-13

```
Alignment Scores:
Pred. No.: 127 Length: 1763
Score: 51.00 Matches: 9
Percent Similarity: 72.22% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 38.64% Indels: 0
DB: 6 Gaps: 0
```

US-09-632-036F-6 (1-24) x US-10-632-150-13 (1-1763)

```
Qy 3 HisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
```

```
Db 1567 CACAATCAGAAATAACACTCGAGATCAGACCCCAAGGAGTGACATCTGTAGT 1514
```

RESULT 10

US-11-073-457-13/c

```
/ Sequence 13, Application US/11073457
```

```
/ Publication No. US20050260556A1
```

GENERAL INFORMATION:

```
/ APPLICANT: Pagano, M.
```

```
/ TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
```

```
/ FILE REFERENCE: 5914-090-999
```

```
/ CURRENT APPLICATION NUMBER: US/11/073,457
```

```
/ CURRENT FILING DATE: 2005-03-04
```

```
/ PRIOR APPLICATION NUMBER: 10/042,417
```

```
/ PRIOR FILING DATE: 2002-01-07
```

```
/ PRIOR APPLICATION NUMBER: 60/260,179
```

```
/ PRIOR FILING DATE: 2001-01-05
```

```
/ NUMBER OF SEQ ID NOS: 92
```

```
/ SOFTWARE: Patent in Ver. 2.0
```

```
/ SEQ ID NO 13
```

```
/ LENGTH: 1763
```

```
/ TYPE: DNA
```

```
/ ORGANISM: Homo sapiens
```

US-11-073-457-13

```
Alignment Scores:
Pred. No.: 127 Length: 1763
Score: 51.00 Matches: 9
Percent Similarity: 72.22% Conservative: 4
Best Local Similarity: 50.00% Mismatches: 5
Query Match: 38.64% Indels: 0
DB: 7 Gaps: 0
```

US-09-632-036F-6 (1-24) x US-11-073-457-13 (1-1763)

```
Qy 3 HisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
```



```
Db      1567 CACAAATCAGAAATAAACAACACTCGAGATCAGACACCCCAAGGAGTGACATCTGTAGT 1514
RESULT 11
US-11-074-176-257/c
; Sequence 257, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Accarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1794)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1763; oligopeptidase
US-11-074-176-257
Alignment Scores:
Pred. No.:      130      Length:      1794
Score:          51.00    Matches:      13
Percent Similarity: 68.18% Conservative: 2
Best Local Similarity: 59.09% Mismatches: 5
Query Match:     38.64% Indels: 2
DB:              7      Gaps: 2
US-09-632-036F-6 (1-24) x US-11-074-176-257 (1-1794)
Qy      2 LeuHieasnGlnGluValThrAlaGluaspGlyThrGlnArgAlaGlu---LysCysSer 20
Db      859 CTACATACCGTGAAGTAAAT---CAAGATGGGAGTCAACTTTCGAATCAAAAGTGTGCT 803
Qy      21 LysPro 22
Db      802 AAACCT 797
RESULT 12
US-11-082-389-249/c
; Sequence 249, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Habethauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
US-09-632-036F-6 (1-24) x US-11-082-389-249 (1-780)
Qy      6 GluValThrAlaGluaspGlyThrGlnArgAlaGluLys-----CysSerLysPro 22
Db      585 GAGTCACGCGCGCGAGGGGTTCTCGAAGCAATAAGCGCGCTTTCGCTAAACCT 526
Qy      23 CysAla 24
Db      525 TGGCT 520
RESULT 13
US-10-750-185-55939
; Sequence 55939, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 55939
; LENGTH: 2766
; TYPE: DNA
; ORGANISM: Bovine 19866881077767
US-10-750-185-55939
Alignment Scores:
Pred. No.:      405      Length:      2766
```

```
Score: 49.50 Matches: 13
Percent Similarity: 69.57% Conservative: 3
Best Local Similarity: 56.52% Mismatches: 5
Query Match: 37.50% Indels: 2
DB: 6 Gaps: 1
US-09-632-036F-6 (1-24) x US-10-750-185-55939 (1-2766)

QY 1 ProLeuHisAsnGlnGluValThrAlaGlu-AspGlyThrGlnArgAlaGluLysCysSe 20
||||| :||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2067 CCACTTCAGACAGTGA---ACGGCAAAACCAAGCAGGAGGGTAGACTGTGTTTC 2123
QY 20 rLysPro 22
|||||:|||||:
Db 2124 AAAGCCA 2130

RESULT 14
US-11-121-086-17
; Sequence 17, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 178877
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-17

Alignment Scores:
Pred. No.: 6.93e+04 Length: 178877
Score: 49.50 Matches: 9
Percent Similarity: 71.43% Conservative: 6
Best Local Similarity: 42.86% Mismatches: 5
Query Match: 37.50% Indels: 1
DB: 7 Gaps: 1
US-09-632-036F-6 (1-24) x US-11-121-086-17 (1-178877)

QY 4 AsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCys 23
Db 96206 AACAGGCAACTCACT---CAAGAAGGAATACACAGGGCCAATAAATGTATGAAAGTTGC 96262
QY 24 Ala 24
:::
Db 96263 TCA 96265

RESULT 15
US-10-750-185-1366/c
; Sequence 1366, Application US/10750185
; Publication No. US2005026603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1366
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT14603
US-10-750-185-1366

Alignment Scores:
Pred. No.: 74.9 Length: 600
Score: 49.00 Matches: 9
Percent Similarity: 59.09% Conservative: 4
Best Local Similarity: 40.91% Mismatches: 7
Query Match: 37.12% Indels: 2
DB: 6 Gaps: 1
US-09-632-036F-6 (1-24) x US-10-750-185-1366 (1-600)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 365 CCCCTGCATGGGCAAGATGTGACCATGCTGCT-----ATAAACACAGCTGTGCT 312
QY 21 LysPro 22
:::|
Db 311 CGCCCA 306

RESULT 16
US-11-121-086-3
; Sequence 3, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 168516
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-3

Alignment Scores:
Pred. No.: 7.86e+04 Length: 168516
Score: 49.00 Matches: 9
Percent Similarity: 54.17% Conservative: 4
Best Local Similarity: 37.50% Mismatches: 11
Query Match: 37.12% Indels: 0
DB: 7 Gaps: 0
US-09-632-036F-6 (1-24) x US-11-121-086-3 (1-168516)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 33457 CCCCTACACTCCATGACCTGTCCTGACCCAGGCTCCCGACGAGCAGCCACATGCTCC 33516
QY 21 LysProCysAla 24
|||
Db 33517 AGCCCCACGGCC 33528

RESULT 17
US-11-121-086-69/c
; Sequence 69, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
```

```
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 190882
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-69

Alignment Scores:
Pred. No.:          9.16e+04      Length:      190882
Score:              49.00         Matches:      9
Percent Similarity: 60.87%        Conservative: 5
Best Local Similarity: 39.13%      Mismatches:  0
Query Match:        37.12%        Indels:      0
DB:                 7            Gaps:         0

US-09-632-036F-6 (1-24) x US-11-121-086-69 (1-190882)

Qy      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
      |||||
Db 189754 CCACCTGCACCTCCAGCCTGGTGACAGAGGAGATTCTCTCAAAAAAAAAAGAGATGCGCTG 189695

Qy      21 LysProCys 23
      |||
Db 189694 TGTCTGTGC 189686

RESULT 18
US-10-750-185-61160
; Sequence 61160, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61160
; LENGTH: 1430
; TYPE: DNA
; ORGANISM: Bovine 19866880738483
US-10-750-185-61160

Alignment Scores:
Pred. No.:          327          Length:      1430
Score:              48.00         Matches:      8
Percent Similarity: 66.67%        Conservative:  4
Best Local Similarity: 44.44%      Mismatches:  6
Query Match:        36.36%        Indels:      0
DB:                 6            Gaps:         0

US-09-632-036F-6 (1-24) x US-10-750-185-61160 (1-1430)

Qy      7 ValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCysAla 24
      |||||
Db 374 GTCTGTCGACGAGTGGAGCTACAAAGCTGAAAGAGCTCCACAGCCCTCTCC 427

RESULT 19
US-10-750-185-41622

; Sequence 41622, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41622
; LENGTH: 1795
; TYPE: DNA
; ORGANISM: Bovine 19866880973184
US-10-750-185-41622

Alignment Scores:
Pred. No.:          432          Length:      1795
Score:              48.00         Matches:      9
Percent Similarity: 60.00%        Conservative:  3
Best Local Similarity: 45.00%      Mismatches:  8
Query Match:        36.36%        Indels:      0
DB:                 6            Gaps:         0

US-09-632-036F-6 (1-24) x US-10-750-185-41622 (1-1795)

Qy      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
      |||||
Db 189 CCCCCCACCACCCAGCCCTCAGGTCAATGGAGCTCTAGCCAGGAGAAATGTGCA 248

RESULT 20
US-11-121-086-100/c
; Sequence 100, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 100
; LENGTH: 124972
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-100

Alignment Scores:
Pred. No.:          8.11e+04      Length:      124972
Score:              48.00         Matches:      9
Percent Similarity: 52.17%        Conservative:  3
Best Local Similarity: 39.13%      Mismatches: 11
Query Match:        36.36%        Indels:      0
DB:                 7            Gaps:         0

US-09-632-036F-6 (1-24) x US-11-121-086-100 (1-124972)

Qy      1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
      |||||
Db 4340 CCAGTGCATGACCAAGAATATATGGCCTGAGACAGCTGAGACAAGGCTGAGGCATGCGCAA 4281
```

QY 21 LysProCys 23
DB 4280 GGCCAATGT 4272

RESULT 21
US-11-171-086 99/c
; Sequence 99, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99
; LENGTH: 134174
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-99

Alignment Scores:
Pred. No.: 8 85e+04 Length: 134174
Score: 48.00 Matches: 9
Percent Similarity: 52.17% Conservative: 3
Best Local Similarity: 39.13% Mismatches: 11
Query Match: 36.36% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-121-086-99 (1-134174)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 109403 CCAGTGCATGACCAAGAATATATGGCTGAGACAGCTGAGACAAGGGTGAGGCATGCCAA 109344

QY 21 LysProCys 23
DB 109343 GGCCAATGT 109335

RESULT 22
US-10-750-185-40234
; Sequence 40234, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40234
; LENGTH: 1634
; TYPE: DNA
; ORGANISM: Bovine 19866881082730
US-10-750-185-40234

Alignment Scores:
Pred. No.: 575 Length: 1634
Score: 47.00 Matches: 10
Percent Similarity: 68.75% Conservative: 1

Best Local Similarity: 62.50% Mismatches: 5
Query Match: 35.61% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-750-185-40234 (1-1634)

QY 2 LeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGlu 17
DB 541 CTGCACAGACGAGAAGTGAAGGCAGAGGATAACTGCTGAGGCTGAA 588

RESULT 23
US-11-117-187-211
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
; LENGTH: 1082144
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-211

Alignment Scores:
Pred. No.: 1 54e+06 Length: 1082144
Score: 47.00 Matches: 10
Percent Similarity: 47.83% Conservative: 1
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 35.61% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-117-187-211 (1-1082144)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 860624 CCTTTTCAACGACACATCGCCGATAGCTCGGAACCTCAGAGAAAGGAGAAATACAGT 860683

QY 21 LysProCys 23
DB 860684 CAACCTTGT 860692

RESULT 24
US-10-750-185-54567
; Sequence 54567, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54567
; LENGTH: 1219


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; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 511
; LENGTH: 2668
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-131-826A-511

Alignment Scores:
Pred. No.: 1.57e+03 Length: 2668
Score: 46.00 Matches: 9
Percent Similarity: 50.00% Conservative: 2
Best Local Similarity: 40.91% Mismatches: 11
Query Match: 34.85% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x US-10-131-826A-511 (1-2668)

Qy 2 LeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLys 21
   :::::
Db 2067 GTACACGACGATGCGACGAGGCTAATGACGGCAACATGACCCCATCTACTGCAGCAAG 2008
   :::::

Qy 22 ProCys 23
   :::::
Db 2007 GGCTGT 2002

RESULT 31
US-11-117-187-185
; Sequence 185, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; PRIOR FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 185
; LENGTH: 64415
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: modified base
; LOCATION: (9960)..(21146)
; OTHER INFORMATION: N = A, C G, or T/U
US-11-117-187-185

Alignment Scores:
Pred. No.: 7.97e+04 Length: 64415
Score: 46.00 Matches: 10
Percent Similarity: 47.83% Conservative: 1
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 34.85% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-117-187-185 (1-64415)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
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Db 56937 CCTTTTCAACGACAAATCGACCGCATAGCTCGGAACTCAGAGAAAGGAAAAACACAGT 56996

Qy 21 LysProCys 23
   :::::
Db 56997 CAACCTTGT 57005

RESULT 32
US-11-112-908-24/c
; Sequence 24, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 150314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-24

Alignment Scores:
Pred. No.: 2.24e+05 Length: 150314
Score: 46.00 Matches: 9
Percent Similarity: 61.90% Conservative: 4
Best Local Similarity: 42.86% Mismatches: 8
Query Match: 34.85% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-112-908-24 (1-150314)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
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Db 145200 CCACTGCATCTCCAGCCTAGTGACAGCAAGACTCCGCTCTCAAAAAAAAAAAGT 145141
   |||

Qy 21 Lys 21
   |||
Db 145140 AAA 145138

RESULT 33
US-11-117-187-212/c
; Sequence 212, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 212
; LENGTH: 163317
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-212
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Alignment Scores:
Pred. No.: 2.48e+05 Length: 163317
Score: 46.00 Matches: 10
Percent Similarity: 47.83% Conservative: 1
Best Local Similarity: 43.48% Mismatches: 12
Query Match: 34.85% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-117-187-212 (1-163317)

QY 1 ProLeuHisasnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
DB 96857 CTTTTCACGACGAAACATCGACCACATAGCTCGGAACCTCAGAGAAAGGAGAACACAGT 96798
QY 21 LysProCys 23
DB 96797 CAACCTTGT 96789

RESULT 34
US-11-121-086-16/c
; Sequence 16, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 189539
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-16

Alignment Scores:
Pred. No.: 2.97e+05 Length: 189539
Score: 46.00 Matches: 10
Percent Similarity: 66.67% Conservative: 2
Best Local Similarity: 55.56% Mismatches: 6
Query Match: 34.85% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x US-11-121-086-16 (1-189539)

QY 4 AsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLys 21
DB 117534 AATCAATTCATTCTGCCACTATGGGTATATAAGATCGAGAAATGTTCTAAA 117481

RESULT 35
US-11-121-086-31/c
; Sequence 31, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 218821
; TYPE: DNA
; ORGANISM: Homo sapiens
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/ NAME/KEY: modified_base
/ LOCATION: (106949)..(106949)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (110322)..(110324)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (115133)..(115133)
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/ NAME/KEY: modified_base
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/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (139059)..(139158)
/ OTHER INFORMATION: a, c, g, t, unknown or other
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/ NAME/KEY: modified_base
/ LOCATION: (157740)..(157740)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
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/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (157900)..(157900)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (157919)..(157919)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
/ LOCATION: (157926)..(157926)
/ OTHER INFORMATION: a, c, g, t, unknown or other
/ FEATURE:
/ NAME/KEY: modified_base
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/ OTHER INFORMATION: a, c, g, t, unknown or other
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/ LOCATION: (158138)..(158138)
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/ LOCATION: (158193)..(158195)
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NAME/KEY: modified_base
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NAME/KEY: modified_base
LOCATION: (170247)..(170247)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170249)..(170250)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170252)..(170253)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170259)..(170259)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170262)..(170263)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170266)..(170266)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (174470)..(174470)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (174472)..(174472)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base

LOCATION: (174474)..(174474)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179059)..(179060)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179064)..(179064)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179001)..(179001)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (197004)..(197005)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (197007)..(197007)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (200349)..(200349)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (200351)..(200351)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212425)..(212426)
OTHER INFORMATION: a, c, g, t, unknown or other
FEATURE:
US-11-121-086-31
Alignment Scores:
Pred. No.: 3.53e+05 Length: 218821
Score: 46.00 Matches: 8
Percent Similarity: 69.23% Conservative: 1
Best Local Similarity: 61.54% Mismatches: 4
Query Match: 34.85% Indels: 0
DB: 7 Gaps: 0
US-09-632-036F-6 (1-24) x US-11-121-086-31 (1-218821)
QY 11 AspGlyThrGlnAlaGluLysCysSerLysProCys 23
Db 217811 GAAGGTACACAAATGCCAGTAAGTGCATGAAGAGATGC 217773
RESULT 36
US-11-121-086-27/c
Sequence 27, Application US/11121086
Publication NO. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27
LENGTH: 153142
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-27
Alignment Scores:
Pred. No.: 2.79e+05 Length: 153142

[illegible]

```

; APPLICANT: COPENHAVER, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD:309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 194
; LENGTH: 92584
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-117-187-194

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Alignment Scores:
Pred. No.:      1.85e+05      Length:      92584
Score:          45.00         Matches:      10
Percent Similarity: 47.83%     Conservative: 1
Best Local Similarity: 43.48%   Mismatches:    12
Query Match:      34.09%       Indels:        0
DB:               7           Gaps:          0

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US-09-632-036F-6 (1-24) x US-11-117-187-194 (1-92584)

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Qy      1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db      30841 CCTTTCAACGACAAACATTGACCGCATAGCTCGCGAACTCAGAGAAAAGGAGAAACACAGT 30782
Qy      21 LysProCys 23
Db      30781 GAACCTTGT 30773

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Search completed: December 11, 2005, 03:20:19
Job time : 393.455 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 22:26:14 ; Search time 1957.09 Seconds
(without alignments)
573.755 Million cell updates/sec

Title: US-09-632-036F-6
Perfect score: 132
Sequence: 1 PLHNQEVTAEDGTORAEKCKPKCA 24

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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-DB=EST -QFMT=fastcap -SUFFIX=rst -MINMATCH=0.1 -LOOPCPU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09632036 @CGN 1.1 5432 @runat_02122005_104141_25823 -NCPU=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hic.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gse1.*
10: gb_gse2.*
11: gb_gse3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	97.0	333	7	CN409749
2	128	97.0	356	5	BX479259
3	128	97.0	376	7	CN409731
4	128	97.0	497	5	BX479184
5	128	97.0	566	7	CN409736
6	128	97.0	582	3	BP313449
7	128	97.0	583	3	BP315895

CN409744	170004243	7	CN409744	589	97.0	128	97.0	8
CV571007	oe07g11.y	7	CV571007	618	97.0	128	97.0	9
AI906012	RC-HT105.	7	AI906012	670	97.0	128	97.0	10
CA489534	AGENCOURT	6	CA489534	808	97.0	128	97.0	11
BE746725	601579159	894	BE746725	1005	97.0	128	97.0	12
BX402419	BX402419	5	BX402419	1005	97.0	128	97.0	13
CR592336	full-leng	2004	CR592336	2004	97.0	128	97.0	14
DQ047381	Pan trogl	3444	DQ047381	3444	97.0	128	97.0	15
DQ047380	Homo sapi	3695	DQ047380	3695	97.0	128	97.0	16
DNS511011	HL0202181	748	DNS511011	748	97.0	121	91.7	17
AW370693	QV1-BT026	614	AW370693	614	88.6	117	88.6	18
CV884121	UI-M-FCO-	820	CV884121	820	87.9	116	87.9	19
BG991986	MR2-HT116	455	BG991986	455	87.1	115	87.1	20
CL413651	RPC144 43	519	CL413651	519	86.4	114	86.4	21
CA544382	C0648D06-	539	CA544382	539	86.4	114	86.4	22
CF902067	A0335H03-	682	CF902067	682	86.4	114	86.4	23
CR119637	Reverse s	854	CR119637	854	86.4	114	86.4	24
AK031099	Mus muscu	4323	AK031099	4323	86.4	114	86.4	25
AK083669	Mus muscu	4463	AK083669	4463	86.4	114	86.4	26
CA328613	UI-M-PY0-	795	CA328613	795	83.3	110	83.3	27
BUL150809	AGENCOURT	964	BUL150809	964	82.6	109	82.6	28
CR767843	DKF2p469C	614	CR767843	614	81.8	108	81.8	29
AL701569	DKF2p686A	474	AL701569	474	69.7	92	69.7	30
BF995059	MR2-GN015	490	BF995059	490	64.4	85	64.4	31
BF995204	MR3-GN015	490	BF995204	490	64.4	85	64.4	32
CV349344	MR2-HT116	552	CV349344	552	64.4	85	64.4	33
BM562913	AGENCOURT	1016	BM562913	1016	62.1	82	62.1	34
AI908047	QV-BT161-	115	AI908047	115	56.8	75	56.8	35
BG954969	CM4-CT065	286	BG954969	286	47.7	63	47.7	36
BX336780	BX336780	709	BX336780	709	47.7	63	47.7	37
CW538167	OP_Ba001	1004	CW538167	1004	47.0	62	47.0	38
AL415232	T7_end of	1004	CNS06U0A	1004	47.0	62	47.0	39
BH011016	ep72h09.g	552	BH011016	552	46.6	61	46.6	40
BZ205610	CH230-293	526	BZ205610	526	45.2	61	45.2	41
CA286377	SCGSD204	526	CA286377	526	45.2	60	45.2	42
CA140633	SCJFRT205	601	CA140633	601	45.5	60	45.5	43
CF576665	MCSA203C0	641	CF576665	641	45.5	60	45.5	44
B0829433	LL6in2234	643	B0829433	643	45.5	60	45.5	45
CZ675091	OM_Ba023	668	CZ675091	668	45.5	60	45.5	46
CA070410	SCSGAD100	829	CA070410	829	45.5	60	45.5	47
CD048799	AGENCOURT	1209	CD048799	1209	45.5	60	45.5	48
CO800753	AGENCOURT	743	CO800753	743	44.7	59	44.7	49
BX391706	BX391706	868	BX391706	868	43.9	59	43.9	50
BZ755010	PUPBK25TB	348	BZ755010	348	43.9	58	43.9	51
CG743040	ZMWBR019	388	CG743040	388	43.9	58	43.9	52
AI635339	tz80h12.x	804	AI635339	804	43.9	58	43.9	53
CF553201	AGENCOURT	856	CF553201	856	43.9	58	43.9	54
AG848401	Oryza sat	874	AG848401	874	43.9	58	43.9	55
BQ965994	QHB23K05.	149	BQ965994	149	43.2	57	43.2	56
BB765881	BB765881	405	BB765881	405	43.2	57	43.2	57
BB675006	BB675006	427	BB675006	427	43.2	57	43.2	58
BB676604	BB676604	427	BB676604	427	43.2	57	43.2	59
CZ412019	1007722 R	535	CZ412019	535	43.2	57	43.2	60
BG825937	602748060	751	BG825937	751	43.2	57	43.2	61
BU253274	603747073	755	BU253274	755	43.2	57	43.2	62
BF262437	HV_CBA000	848	BF262437	848	43.2	57	43.2	63
BI601086	603249577	910	BI601086	910	43.2	57	43.2	64
BZ868523	CH240_226	328	BZ868523	328	42.4	56	42.4	65
AQ035868	CIT-HSP-2	353	AQ035868	353	42.4	56	42.4	66
BB669924	BB669924	400	BB669924	400	42.4	56	42.4	67
BJ661324	BB661324	651	BJ661324	651	42.4	56	42.4	68
CV662265	LCPE04EX0	805	CV662265	805	42.4	56	42.4	69
BI818940	603037434	815	BI818940	815	42.4	56	42.4	70
BZ980494	PUGIW79TD	844	BZ980494	844	42.4	56	42.4	71
CNS011EP	AL145634 Anophel	953	CNS011EP	953	42.4	56	42.4	72
AQ694702	HS 5473 B	476	AQ694702	476	42.0	55	42.0	73
CL861864	OR_CBA009	783	CL861864	783	42.0	55	42.0	74
BO539210	MEST612-E	356	BO539210	356	41.7	55	41.7	75
BB677696	BB677696	434	BB677696	434	41.7	55	41.7	76
BQ869495	QGD6F13.y	559	BQ869495	559	41.7	55	41.7	77
BJ037389	BJ037389	566	BJ037389	566	41.7	55	41.7	78
AI677624	605057H06	585	AI677624	585	41.7	55	41.7	79
AU035223	AU035223	587	AU035223	587	41.7	55	41.7	80

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81 55 41.7 609 3 BI839047
82 55 41.7 658 7 CF950469 UI-M-HL0-
C 83 55 41.7 663 5 BY752074
C 84 55 41.7 664 3 BM339638
85 55 41.7 668 3 BJ666137
86 55 41.7 708 9 BZ415417
87 55 41.7 753 10 CG102034
88 55 41.7 830 7 CO960399
C 89 55 41.7 836 9 BZ980491
C 90 55 41.7 840 8 DR785590
91 55 41.7 864 2 BG320282
92 55 41.7 913 11 CNS033KP
93 55 41.7 1496 4 BC075711
94 54.5 41.3 435 2 BI051584
95 54.5 41.3 588 6 CD890987
96 54.5 41.3 616 6 CD925860
C 97 54.5 41.3 619 2 BE162709
C 98 54.5 41.3 650 10 AG019503
C 99 54.5 41.3 780 9 CC143331
C 100 54.5 41.3 956 2 BG033293

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ALIGNMENTS

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LOCUS 17000532194973 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN409749
VERSION CN409749.1 GI:47396873
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 333)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBLISHED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
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FEATURES
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Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, embryoid bodies
derived from H1, H7 and H9 cells"
/clone_lib="GRN_EB"
/notes="oligo dt primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hes cell lines
H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."

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ORIGIN

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Alignment Scores:
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Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

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US-09-632-036F-6 (1-24) x CN409749 (1-333)
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Db 69 CCCCTGCAACCAAGAGGTGACAGAGGATGACACACGCGGTGTGAGAAGTGCAGC 128
QY 21 LysProCysAla 24
Db 129 AAGCCCTGTGCC 140

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RESULT 2

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BX479259 356 bp mRNA linear EST 04-SEP-2003
DKFZp686M18209 r1 686 (synonym: hicc3) Homo sapiens cDNA clone
DKFZp686M18209 5', mRNA sequence.
ACCESSION BX479259
VERSION BX479259.1 GI:31914879
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 356)
AUTHORS Bloeker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Bloeker,H., Boecher,M., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No s1 sequence available.
This clone (DKFZp686M18209) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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Location/Qualifiers
1..356
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686M18209"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hicc3)"
/notes="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

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ORIGIN

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Alignment Scores:
Pred. No.: 5.25e-10 Length: 356
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 5 Gaps: 0
US-09-632-036F-6 (1-24) x BX479259 (1-356)

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QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 172 CCCCTGCAACCAAGAGGTGACAGAGGATGACACACGCGGTGTGAGAAGTGCAGC 231
QY 21 LysProCysAla 24
Db 232 AAGCCCTGTGCC 243

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RESULT 3
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 LOCUS 17000532198194 GRN_EB Homo sapiens cDNA 5', mRNA sequence. EST 16-MAY-2004
 DEFINITION
 CN409731
 ACCESSION
 VERSION
 CN409731.1 GI:47396855
 KEYWORDS
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 376)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: tbrandenberger@geron.com
 Insert Length: 376 Std Error: 0.00.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryoid bodies
 derived_from H1, H7 and H9 cells"
 /clone_lib="GRN_EB"
 /note="oligo dt primed, full-length enriched cDNA library
 from embryoid body outgrowths derived from HES cell lines
 H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
 conditions."

Alignment Scores:
 Pred. No.: 5.6e-10 Length: 376
 Score: 128.00 Matches: 23
 Percent Similarity: 95.83% Conservative: 0
 Best Local Similarity: 95.83% Mismatches: 1
 Query Match: 96.97% Indels: 0
 DB: 7 Gaps: 0

ORIGIN

US-09-632-036F-6 (1-24) x CN409731 (1-376)
 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
 |||||
 188 CCCCTGCACCAACAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAGTGCAGC 247
 |||||
 21 LysProCysAla 24
 |||||
 248 AGCCCTGTGCC 259
 |||||

RESULT 4
 BX479184
 LOCUS 17000532198194 GRN_EB Homo sapiens cDNA 5', mRNA sequence. EST 04-SEP-2003
 DEFINITION
 BX479184
 ACCESSION
 VERSION
 BX479184.1 GI:31914729
 KEYWORDS
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE

AUTHORS
 1 (bases 1 to 497)
 Bloecker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,
 Fobo, G., Han, M. and Wiemann, S.
 EST [Bloecker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.]
 JOURNAL
 Unpublished (2003)
 COMMENT
 Contact: MIPS
 MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by GfR (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.

This clone (DKFZp686G01209) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
 1..497
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp686G01209"
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 /lab_host="DH10B"
 /clone_lib="686 (synonym: hlcc3)"
 /note="Vector: pTriplex2; Site_1: SfIIA; Site_2: SfiIB;
 cDNA-collection"

ORIGIN

Alignment Scores:
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 Score: 128.00 Matches: 23
 Percent Similarity: 95.83% Conservative: 0
 Best Local Similarity: 95.83% Mismatches: 1
 Query Match: 96.97% Indels: 0
 DB: 5 Gaps: 0

US-09-632-036F-6 (1-24) x BX479184 (1-497)

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 |||||
 171 CCCCTGCACCAACAGAGGTGACAGCAGAGGATGGAAACACAGCGGTGTGAGAGTGCAGC 230
 |||||
 21 LysProCysAla 24
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 231 AAGCCCTGTGCC 242
 |||||

RESULT 5

CN409736
 LOCUS 17000532198194 GRN_EB Homo sapiens cDNA 5', mRNA sequence. EST 16-MAY-2004
 DEFINITION
 CN409736
 ACCESSION
 VERSION
 CN409736.1 GI:47396860
 KEYWORDS
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

REFERENCE
 1 (bases 1 to 566)
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
 Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
 Lebkowski, J. and Stanton, L.W.
 Transcriptionome characterization elucidates signaling networks that
 control human ES cell growth and differentiation
 Nat. Biotechnol. 22 (6), 707-716 (2004)
 15146197
 Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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FEATURES

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 derived from H1, H7 and H9 cells"
 /clone_lib="GRN EB"
 /notes="Oligo dT primed, full-length enriched cDNA library
 from embryoid body outgrowths derived from hES cell lines
 H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free
 conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 9,04e-10 Length: 566
 Score: 128.00 Matches: 23
 Percent Similarity: 95.83% Conservative: 0
 Best Local Similarity: 95.83% Mismatches: 1
 Query Match: 96.97% Indels: 0
 DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CN409736 (1-566)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAapGlyThrGlnArgAlaGluLysCysSer 20
 DB 412 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACGCGGTGTGAGAAGTGCAGC 471
 QY 21 LysProCysAla 24
 DB 472 AAGCCCTGTGCC 483

RESULT 6

LOCUS BP313449 582 bp mRNA linear EST 17-SEP-2004
 DEFINITION BP313449 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
 CDNA clone OFR03249, mRNA sequence.

ACCESSION BP313449
 VERSION BP313449.1 GI:52242424
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 582)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1..582

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="OFR03249"

/tissue_type="mammary gland"

/cell_line="OCUB-F"

/clone_lib="Sugano cDNA library, mammary gland OCUB-F"

/note="mammary gland tumor"

ORIGIN

Alignment Scores:

Pred. No.: 9,34e-10 Length: 582
 Score: 128.00 Matches: 23
 Percent Similarity: 95.83% Conservative: 0
 Best Local Similarity: 95.83% Mismatches: 1
 Query Match: 96.97% Indels: 0
 DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x BP313449 (1-582)

QY 1 ProLeuHisAenGlnGluValThrAlaGluAapGlyThrGlnArgAlaGluLysCysSer 20
 DB 363 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACGCGGTGTGAGAAGTGCAGC 422
 QY 21 LysProCysAla 24
 DB 423 AAGCCCTGTGCC 434

RESULT 7

LOCUS BP315895 583 bp mRNA linear EST 17-SEP-2004
 DEFINITION BP315895 Sugano cDNA library, mammary gland OCUB-F Homo sapiens
 CDNA clone OFR09650, mRNA sequence.

ACCESSION BP315895
 VERSION BP315895.1 GI:52244870
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.

REFERENCE 1 (bases 1 to 583)

AUTHORS Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,

Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

CONTACT: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

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/cell_line="OCUB-F"

/clone_lib="Sugano cDNA library, mammary gland OCUB-F"

/note="mammary gland tumor"

ORIGIN

Alignment Scores:
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 Score: 128.00 Matches: 23
 Percent Similarity: 95.83% Conservative: 0
 Best Local Similarity: 95.83% Mismatches: 1
 Query Match: 96.97% Indels: 0
 DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x BP315895 (1-583)

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 DB 415 CCCCTGCACACCAAGAGGTGACAGCAGAGGTGGAACACACGCGGTGTGAGAAGTGCAGC 474
 QY 21 LysProCysAla 24
 DB 475 AAGCCCTGTGCC 486


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RESULT 8
LOCUS      CN409744
DEFINITION 589 bp mRNA linear EST 16-MAY-2004
ACCESSION 17000424385945 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
VERSION    CN409744
KEYWORDS   CN409744.1 GI:47396868
SOURCE     EST.
ORGANISM   Homo sapiens (human)
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 589)
AUTHORS    Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
            Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
            Lebkowski, J. and Stanton, L.W.
TITLE      Transcriptional characterization elucidates signaling networks that
JOURNAL    control human ES cell growth and differentiation
PUBMED     Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT    15146197
            Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
FEATURES   source
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            /mol_type="mRNA"
            /db_xref="taxon:9606"
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            H9"
            /clone_lib="GRN_ES"
            /note="oligo dt primed, full-length enriched cDNA library
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            and H9 (p26) maintained in feeder-free conditions"

ORIGIN
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Pred. No.: 9,48e-10 Length: 589
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CN409744 (1-589)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 453 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCGAGC 512

Qy 21 LysProCysAla 24
Db 513 AAGCCCTGTGCC 524

RESULT 9
CV571007
LOCUS      CV571007
DEFINITION 618 bp mRNA linear EST 22-OCT-2004
ACCESSION CV571007
KEYWORDS   CV571007.1 GI:54472119
SOURCE     sapiens cDNA clone oe07g11 5', mRNA sequence.
ORGANISM   Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 618)

Rabinowitz, Y., Dong, L. and Wistow, G.
Expressed sequence tag analysis of human keratoconus cornea
Unpublished (2004)
Contact: Wistow G
Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
Email: graeme@helix.nih.gov
Plate: 07 row: g column: 11
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..618
/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="Cornea"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human keratoconus cornea, unamplified,
(od/oe)"
/note="Organ: Eye; Vector: pCMVSPORT6; Approximately 40ug
total RNA was extracted from 7 adult human keratoconus
corneas. A directionally cloned cDNA library in the
pSPORT1 vector (Invitrogen) was constructed at Bioserve
Biotechnology (Laurel MD) essentially following the
protocols of the SuperScript Plasmid System full details
of which are contained in the manufacturer's instruction
manual (http://www.lifetech.com/). First strand synthesis
was carried out using a Not I primer-adaptor
[5'-pCAGTAGTTCCTAGATCGAGCGGCCG(T)15-3']. cDNA was
cloned in Not I/Sal I sites. EST analysis was performed on
the unamplified library at the NIH Intramural Sequencing
Center (NISC)."

ORIGIN
Alignment Scores:
Pred. No.: 1e-09 Length: 618
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CV571007 (1-618)

Qy 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 25 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGGAACACACAGCGGTGTGAGAGTGCGAGC 84

Qy 21 LysProCysAla 24
Db 85 AAGCCCTGTGCC 96

RESULT 10
AI906012/c
LOCUS      AI906012/c
DEFINITION RC-BT105-110399-035 BT105 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI906012
VERSION    AI906012.1 GI:6496399
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE  1 (bases 1 to 670)
AUTHORS    Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R.,
            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
            Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
            Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

```

O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

TITLE

JOURNAL

PUBLISHED

COMMENT

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/seq/gethtml.pl?cl=RC&t2=RC-BT105-035.html

&t3=il0399&t4=1)

Seq primer: puc 18 forward.

Location/Qualifiers

FEATURES

source

1..670

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/sex="female"

/dev_stage="Adult"

/clone_lib="BT105"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:

SmaI; A mini-library was made by cloning products derived

from ORFEST PCR (U.S. Letters Patent application No.

196,716 - Ludwig Institute for Cancer Research) profiles

into the pUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.: 1..1e-09 Length: 670

Score: 128.00 Matches: 23

Percent Similarity: 95.83% Conservative: 0

Best Local Similarity: 95.83% Mismatches: 1

Query Match: 96.97% Indels: 0

DB: 1 Gaps: 0

US-09-632-036F-6 (1-24) x AI906012 (1-670)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

|||||

Db 157 CCCCTGCACCAACCAAGAGGTGACACGAGGATGGAAACACACGCGGTGAGAGTGCAGC 98

|||||

QY 21 LysProCysAla 24

|||||

Db 97 AAGCCCTGTGCC 86

|||||

RESULT 11

CA489534

AGENCOURT_10810594 MAPcL Homo sapiens cDNA clone IMAGE:6722008 5',

mRNA sequence.

CA489534 808 bp mRNA linear EST 14-NOV-2002

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

1 (bases 1 to 808)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Kristi A. Eglund, Ira Pastan

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

cDNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM14284 row: a column: 16

High quality sequence stop: 582.

Location/Qualifiers

1..808

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6722008"

/cell_lines="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,

hTERT-HME1, LNCaP"

/lab_host="EMDH10B"

/clone_lib="MAPcL"

/note="Vector: pCMV-SPORT6; Site 1: EcoRV; Site 2: Not I;

Subtracted with brain, liver, lung, kidney and muscle.

Directionally cloned. Priming method: oligo-dT. Average

insert size: 1800 bp. Library amplification: 26,000 fold.

Kristi A. Eglund, James J. Vincent, Robert Strausberg,

Bungkook Lee & Ira Pastan: Discovery of new breast

cancer genes encoding membrane and secreted proteins.

Manuscript submitted."

Alignment Scores:

Pred. No.: 1.37e-09 Length: 808

Score: 128.00 Matches: 23

Percent Similarity: 95.83% Conservative: 0

Best Local Similarity: 95.83% Mismatches: 1

Query Match: 96.97% Indels: 0

DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CA489534 (1-808)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

|||||

Db 552 CCCCTGCACCAACCAAGAGGTGACACGAGGATGGAAACACACGCGGTGAGAGTGCAGC 611

|||||

QY 21 LysProCysAla 24

|||||

Db 612 AAGCCCTGTGCC 623

|||||

RESULT 12

BE746725

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

1 (bases 1 to 894)

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCW758 row: e column: 16

High quality sequence start: 3
High quality sequence stop: 762.

FEATURES

source
1..894
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="IMAGE:3927927"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: Ovary; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:
Pred. No.: 1.55e-09 Length: 894
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x BE746725 (1-894)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 260 CCCCTGCACAAACGAGGTGACAGCAGAGGTGGAACACAGCGGTGTGAGAGTGCAGC 319
QY 21 LysProCysAla 24
Db 320 AAGCCCTGTGCC 331

RESULT 13

BX402419
LOCUS
DEFINITION
BX402419 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI032YB05 5-PRIME, mRNA sequence.

ACCESSION
BX402419

VERSION
BX402419.2 GI:46922471

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1005)

AUTHORS
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE
Full-length cDNA libraries and normalization

JOURNAL
Unpublished (2001)

COMMENT
On May 13, 2003 this sequence version replaced gi:30632074.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 8568.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?as=CSIAI008ZH03QP1&c=8568.f.

FEATURES

source

1..1005

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="CSODI032YB05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 1.77e-09 Length: 1005
Score: 128.00 Matches: 23
Percent Similarity: 95.83% Conservative: 0
Best Local Similarity: 95.83% Mismatches: 1
Query Match: 96.97% Indels: 0
DB: 5 Gaps: 0

US-09-632-036F-6 (1-24) x BX402419 (1-1005)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20

Db 435 CCCCTGCACAAACGAGGTGACAGCAGAGGTGGAACACAGCGGTGTGAGAGTGCAGC 494

QY 21 LysProCysAla 24

Db 495 AAGCCCTGTGCC 506

RESULT 14

CR592336

LOCUS

DEFINITION

CR592336

full-length cDNA clone CSODI032YB05 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION

CR592336

VERSION

CR592336.1 GI:50473143

KEYWORDS

HTC; CNSLT.CDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homnidae; Homo.

REFERENCE

1 (bases 1 to 2004)

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue

Genoscope.

REFERENCE

2 (bases 1 to 2004)

AUTHORS

Direct Submission

TITLE

Submitted (20-JUL-2004)

JOURNAL

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

FEATURES

Location/Qualifiers

source

1..2004

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CSODI032YB05"

/tissue_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 3.99e-09 Length: 2004

Score: 128.00 Matches: 23

Percent Similarity: 95.83% Conservative: 0


```

/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FC0"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonalido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAGAGAGCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP): 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

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ORIGIN

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Alignment Scores:
Pred. No.: 1,11e-07 Length: 820
Score: 116.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 87.88% Indels: 0
DB: Gaps: 0

```

US-09-632-036F-6 (1-24) x CV884121 (1-820)

```

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| :|||
Db 30 CCCCGAACACACAGAGGTGCACAGCTGAGGACGACACACGCGTGTGAGAAATGCAGC 89
||| :|||
QY 21 LysProCysAla 24
||| :|||
Db 90 AAGCCCTGTGCT 101
||| :|||

```

```

RESULT 20
BG991986/c
LOCUS BG991986 455 bp mRNA linear EST 13-JUN-2001
DEFINITION MR2-HT1163--310101-016-f04 HT1163 Homo sapiens cDNA, mRNA sequence.
ACCESSION BG991986
VERSION BG991986.1 GI:14396056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

```

```

REFERENCE 1 (bases 1 to 455)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Ngai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

```

```

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

```

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?cl=MR2&t2=MR2-HT1163->

```

310101-016-f04&r3=2001-01-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 454.
Location/Qualifiers

```

FEATURES

source

```

1..455
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1163"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN

```

Alignment Scores:
Pred. No.: 8.02e-08 Length: 455
Score: 115.00 Matches: 23
Percent Similarity: 92.00% Conservative: 0
Best Local Similarity: 92.00% Mismatches: 1
Query Match: 87.12% Indels: 1
DB: Gaps: 0

```

US-09-632-036F-6 (1-24) x BG991986 (1-455)

```

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSe 20
||| :|||
Db 126 CCCCTGCACACACAGAGGTGCACAGCAGAGGTGGAACACACGCGTGTGAGAGTGCAG 67
||| :|||
QY 20 LysProCysAla 24
||| :|||
Db 66 CAAGCCCTGTGCC 54
||| :|||

```

RESULT 21

CL413651

```

LOCUS RPI44_433J16.r RPI44-44 Sub scrofa genomic clone RPI44_433J16,
DEFINITION genomic survey sequence.
ACCESSION CL413651
VERSION CL413651.1 GI:51447711
KEYWORDS GSS.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

```

```

REFERENCE 1 (bases 1 to 419)
AUTHORS Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M.,
Beaver,J.E. and Schook,L.B.
TITLE Piggy-BACing the Human Genome: Constructing a Porcine Physical Map
Through Comparative Genomics
JOURNAL Unpublished (2004)
COMMENT Contact: Lawrence B. Schook
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 265 5326
Fax: 217 244 5617
Email: schook@uiuc.edu

```

Clones are derived from the porcine BAC library RPI44-44
(<http://www.bacpac.chori.org/porcine242.htm>). For BAC library
availability, please contact Pieter de Jong (pdejong@chori.org).
Clones may be purchased from BACPAC Resources
(<http://BACPACorders.chori.org>). This work was undertaken as part
of the International Swine Genome Sequencing Consortium by
University of Illinois at Urbana Champaign, USA with funds provided
by grant No. AG2002-34480-11828 from USDA-CSREES and
AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
Initiative)

Plate: 433 row: J column: 16
Seq primer: SP6
Class: BAC ends.

FEATURES

source

Location/Qualifiers

1..419
/organism="Sus scrofa"
/mol_type="genomic DNA"
/strain="Four pigs (breed: 37.5% Yorks Landrace and 25% Meishan)"
/db_xref="taxon:9823"
/clone="RPC144_433J16"
/sex="male"
/cell_type="blood"
/clone_lib="RPC1-44"
/notes="Vector: pTARBAC2; Site 1: EcoRI; Site 2: EcoRI; porcine male BAC library produced by Pieter de Jong"

ORIGIN

Alignment Scores:
Pred. No.: 1,05e-07 Length: 419
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 10 Gaps: 0

US-09-632-036F-6 (1-24) x CL413651 (1-419)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| :|||
Db 117 CCCCCGAAACCAACGAGGTGACAGCTGAGGACGCGGAGCGGTGTGAGAAATGCAGC 176
QY 21 LysProCysAla 24
|||
Db 177 AAGCCCTGTGCC 188

RESULT 22

CA544382 539 bp mRNA linear EST 19-NOV-2002
LOCUS C0648D06-5N NIA Mouse Trophoblast Stem Cell cDNA Library (Long) Mus
DEFINITION musculus cDNA clone NIA:C0648D06 IMAGE:30024809 5', mRNA sequence.

CA544382 1 GI:25087132

EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Luo, A.,
Tanaka, T., Kunath, T., Rossant, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Trophoblast Stem Cell cDNA Library
(Long)

JOURNAL

Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Casseil Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgon.grc.nia.nih.gov
Plate: C0648 row: D column: 06
Seq primer: M13 Reverse
High quality sequence stop: 539
POLYA=No.

FEATURES

source

Location/Qualifiers

1..539
/organism="Mus musculus"
/mol_type="mRNA"
/strain="B5/EGFP transgenic ICR mice"
/db_xref="niaEST:C0648D06-5N"
/db_xref="taxon:10090"
/clone="NIA:C0648D06 IMAGE:30024809"
/tissue_type="Trophoblast stem cell"

/dev_stage="3.5-dpc"
/lab_host="DH10B"
/clone_lib="NIA Mouse Trophoblast Stem Cell cDNA Library
(Long)"
/notes="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgon.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Dr. Janet Rossant and Tilo Kunath (Samuel
Lunenfeld Research Institute, Canada). Double-stranded
cDNAs were synthesized with an Oligo(dT) primer
(Invitrogen):
5'-pGACTAGTCTAGATCGAGCGCGCCCTTTT-3' from
4 ug of total RNA, treated with T4 DNA polymerase, and
purified by ethanol-precipitation. The cDNAs were ligated
to lone-linker LL-Sal4, purified by phenol/chloroform, and
separated from free linkers by Centricon 100. Then, the
cDNAs were amplified by long-range high fidelity PCR using
Ex Taq polymerase (Takara) with a primer Sal4-S. The
products were purified by phenol/chloroform and Centricon
100. The cDNAs were digested with SalI and NotI enzymes
and cloned into SalI/NotI site of pSPORT1 plasmid vector.
The DH10B E. coli host was transformed with the ligation
mixture by the standard chemical method. The average
insert size is about 2.6 kb. The library was constructed
by Yulan Piao (NIA)."

ORIGIN

Alignment Scores:
Pred. No.: 1,41e-07 Length: 539
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CA544382 (1-539)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| :|||
Db 31 CCCCCGAAACCAACGAGGTGACAGCGGAGCGGAGCGGTGTGAGAAATGCAGC 90

QY 21 LysProCysAla 24
|||
Db 91 AAGCCCTGTGCT 102

RESULT 23

CF902067
LOCUS A0335H03-5 NIA Mouse Trophoblast Stem Cell cDNA Library (Long 1)
DEFINITION Mus musculus cDNA clone NIA:A0335H03 IMAGE:30736598 5', mRNA
sequence.

CF902067 1 GI:38169116

EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method
Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL

Unpublished (2001)
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Casseil Drive, Suite 4000, Baltimore, MD 21224-6820, USA

```

Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0335 row: H column: 03
Seq primer: M13 Reverse
High quality sequence stop: 682
POLYA=no.

FEATURES
    source
        1..682
            /organism="Mus musculus"
            /mol_type="mRNA"
            /strain="B5/EGFP transgenic ICR mice"
            /db_xref="niaEST:A0335H03-5"
            /db_xref="taxon:10090"
            /clone="NIA:A0335H03 IMAGE:30736598"
            /dev_stage="3.5-dpc"
            /lab_host="DH10B"
            /clone_lib="NIA Mouse Trophoblast Stem Cell cDNA Library (long 1)"
            /notes="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were obtained from Dr. Janet Rossant and Tilo Kunath (Samuel Lunenfeld Research Institute, Canada). Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen): 5'-pGACTAGTCTAGATCGGAGCGCGCCCTTTTCTTTT-3' from 4 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Loner-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.6 kb. The library was constructed by Yulan Piao."

ORIGIN
Alignment Scores:
Pred. No.: 1..86e-07 Length: 682
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CF902067 (1-682)

QY 1 ProLeuHisAsnGlnUValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 54 CCCCAGAACCAACAGAGGTTCACGCGGAGGACGGAACACAGCGGTGTGAGAAATGCAGC 113
QY 21 LysProCysAla 24
||| ||||| |||||
Db 114 AAACCCCTGTGCT 125

RESULT 24
CR119637/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CR119637
Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP345a06, genomic survey sequence.
CR119637
GSS: genome survey sequence; M1CER.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ORIGIN
Alignment Scores:
Pred. No.: 1..86e-07 Length: 682
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CRI19637 (1-854)

QY 1 ProLeuHisAsnGlnUValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| ::||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 408 CCCCAGAACCAACAGAGGTTCACGCGGAGGACGGAACACAGCGGTGTGAGAAATGCAGC 349
QY 21 LysProCysAla 24
||| ||||| |||||
Db 348 AAGCCCTGTGCT 337

RESULT 25
AK031099
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK031099
Mus musculus 13 days embryo forelimb cDNA, RIKEN full-length enriched library, clone:5930404N10 product:v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian), full insert sequence.
AK031099
HTC; CAP trapper.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
11042159
3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

```



```

PUBMED
REFERENCE
AUTHORS
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE
JOURNAL
REFERENCE
AUTHORS
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE
JOURNAL
REFERENCE
AUTHORS
Nature 420, 563-573 (2002)
6 (bases 1 to 4323)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
Location/Qualifiers
1. .4323
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM,DB:5930404N10"
/db_xref="taxon:10090"
/clone="5930404N10"
/tissue_type="forelimb"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="13 days embryo"
misc_feature
48..3818
/notes="putative
v-erb-b2 erythroblastic leukemia viral oncogene homolog 2,
neuro/glioblastoma derived oncogene homolog (avian)
(MGD|MG1:95410, GB|U71126, evidence: BLASTN, 99%,
match=449)"
ORIGIN
Alignment Scores:
Pred. No.: 1.62e-06 Length: 4323
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 4 Gaps: 0
US-09-632-036f-6 (1-24) x AK031099 (1-4323)
QY
1 ProLeuHisAnGlnGluValThrAlaGluAepGlyThrGlnArgAlaGluLysCysSer 20
||||:|||||
996 CCCCCGAACCAACAGAGGTTCACAGCTGAGGACGGAACACAGCGGTGTGAGAAATGCAGC 1055
Db

```

```

QY
21 LysProCysAla 24
|||||
Db
1056 AAGCCCTGTGCT 1067
RESULT 26
AK083669
LOCUS
DEFINITION
Mus musculus 9 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:D030063B12 product:v-erb-b2 erythroblastic
leukemia viral oncogene homolog 2, neuro/glioblastoma derived
oncogene homolog (avian), full insert sequence.
AK083669
AK083669.1 GI:26101404
VERSION
KEYWORDS
HPC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
10349636
2
REFERENCE
3 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohata, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
11076861
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4463)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,M.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,

```

Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://phantom.gsc.riken.jp/.

FEATURES

source

1. .4463
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:D030063B12"
/db_xref="taxon:10090"
/clone="D030063B12"
/tissue_type="whole body"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="9 days embryo"

misc_feature

1. .4463
/note="v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) (MGI:95410, GB|U71126, evidence: BLASTN, 99%, match=449)"

ORIGIN

Alignment Scores:
Pred. No.: 1.68e-06 Length: 4463
Score: 114.00 Matches: 21
Percent Similarity: 91.67% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 2
Query Match: 86.36% Indels: 0
DB: 4 Gaps: 0

US-09-632-036F-6 (1-24) x AK083669 (1-4463)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
||| :|||
Db 996 CCCCAGACACACAGAGGTGACAGCTGAGGACGGAACACAGCGGTGTGAGAAATGCAC 1055
||| :|||

QY 21 LysProCysAla 24
||| :|||

Db 1056 AAGCCCTGTGCT 1067
||| :|||

RESULT 27

CA328613

LOCUS

DEFINITION UI-N-FYO-cda-e-16-0-UI.r1 NIH_BMAP_FYO Mus musculus cDNA clone
IMAGE:6826841 5', mRNA sequence.

ACCESSION CA328613

VERSION CA328613.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers
1. .795
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6826841"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FYO"

/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according

Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

ORIGIN

Alignment Scores:
Pred. No.: 9.55e-07 Length: 795
Score: 110.00 Matches: 20
Percent Similarity: 95.45% Conservative: 1
Best Local Similarity: 90.91% Mismatches: 1
Query Match: 83.33% Indels: 0
DB: 6 Gaps: 0

US-09-632-036F-6 (1-24) x CA328613 (1-795)

QY 3 HisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysPro 22
::: |||
Db 703 AACAAACAGAGGTGACAGCTGAGGACGGAACACAGCGGTGTGAGAAATGCACGACCC 762
||| :|||

QY 23 CysAla 24
||| :|||

Db 763 TGTGCT 768
||| :|||

RESULT 28

BU150809

LOCUS

DEFINITION

AGENCY: 8118591

clone IMAGE:6180101 5', mRNA sequence.

ACCESSION BU150809

VERSION BU150809.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1 (bases 1 to 964)

AUTHORS NIH-MGC

TITLE NIH-MGC

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM13562 row: f column: 06

High quality sequence start: 27
High quality sequence stop: 529.

FEATURES

Location/Qualifiers
1..964
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6180101"
/sex="male"
/tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
/clone_lib="Lupski dorsal root ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
Noti; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTCTTAGATCGGCGCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

ORIGIN

Alignment Scores:
Pred. No.: 1.72e-06 Length: 964
Score: 109.00 Matches: 20
Percent Similarity: 95.24% Conservative: 0
Best Local Similarity: 95.24% Mismatches: 1
Query Match: 82.58% Indels: 0
DB: 5 Gaps: 0

US-09-632-036F-6 (1-24) x BU150809 (1-964)

QY 4 AenGlnGluValThrAlaGluAapGlyThrGlnArgAlaGluLysCysSerLysProCys 23
|||||
Db 33 AACCAAGAGTGACACAGAGGATGGACACACCGGTGTGAGAAGTGCACGACCGCTGT 92
QY 24 Ala 24
|||
Db 93 GCC 95

RESULT 29
CR767843 614 bp mRNA linear EST 23-SEP-2004
LOCUS DKFZp469C0110 r1 469 (synonym: pkid1) Pongo pygmaeus cDNA clone
DEFINITION DKFZp469C0110 5', mRNA sequence.

ACCESSION CR767843
VERSION CR767843.1 GI:52610368

KEYWORDS EST.
SOURCE Pongo pygmaeus (orangutan)

ORGANISM Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pongo.

REFERENCE 1 (bases 1 to 614)

AUTHORS Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Schaipp, A.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.

TITLE Pongo pygmaeus mRNA (Ottenwaelder, B., Obermaier, B.,

Deutschenbaur, S., et al.)

JOURNAL Unpublished (2004)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert. Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix
(Martinsried/Germany) within the cDNA sequencing consortium of the

German Genome Project. This clone (DKFZp469C0110) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469C0110
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers
1..614
/organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469C0110"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSPORT1_Sfi; Site_1: SfiI; Site_2: SfiIb"

ORIGIN

Alignment Scores:
Pred. No.: 1.46e-06 Length: 614
Score: 108.00 Matches: 20
Percent Similarity: 95.24% Conservative: 0
Best Local Similarity: 95.24% Mismatches: 1
Query Match: 81.82% Indels: 0
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CR767843 (1-614)

QY 1 ProLeuHisAsnGlnGluValThrAlaGluAapGlyThrGlnArgAlaGluLysCysSer 20
|||||
Db 552 CCCCTGTCACCAACAGAGGTGACAGCAGAGGACGACACACGCGGTGTGAGAAGTGCAGC 611

QY 21 Lys 21
|||
Db 612 AAG 614

RESULT 30

AL701569

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by GBF (National Research Centre for Biotechnology Ltd.,

Braunschweig/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No si sequence available.

This clone (DKFZp686A19145) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1..474

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source


```

Alignment Scores:
Pred. No.: 0.00493 Length: 490
Score: 85.00 Matches: 17
Percent Similarity: 85.71% Conservatives: 1
Best Local Similarity: 80.95% Mismatches: 3
Query Match: 64.39% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-6 (1-24) x BF995204 (1-490)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 73 CCCCTGCACACCAAGAGGTGACAGCAGAGGATGCAACACAGAGGTGGAGGAGGAGAG 132
Qy 21 Lys 21
Db 133 AAA 135

RESULT 33
CV349344/c
LOCUS CV349344 552 bp mRNA linear EST 24-SEP-2004
DEFINITION MR2-HT1163-130201-013-f02 HT1163 Homo sapiens cDNA, mRNA sequence.
ACCESSION CV349344
VERSION CV349344.1 GI:52672558
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 552)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. http://www.ludwig.org.br.
Location/Qualifiers
1..552
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT1163"
/notes="Organ: head neck; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 0.00567 Length: 552
Score: 85.00 Matches: 18
Percent Similarity: 76.00% Conservatives: 1
Best Local Similarity: 72.00% Mismatches: 5
DB: 1 Gaps: 0

US-09-632-036F-6 (1-24) x BM562913 (1-1016)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCys 20
Db 797 CCCCTGCACACCAAGAGGTGACCGCAGAGATGGAACACACACCGCGTGTGAAAAAGTGCA 856
Qy 20 erLysPro 22
Db 1 Gaps: 0

Query Match: 64.39% Indels: 1
DB: 7 Gaps: 0

US-09-632-036F-6 (1-24) x CV349344 (1-552)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSer 20
Db 122 CCCCTGCACACCAAGAGGTGACAGCAGAGATGGACACACCGCGTGTGAGAGTGCAGC 63
Qy 21 Lys-ProCysAla 24
Db 62 AACGCCCTGTGCC 50

RESULT 34
BM562913
LOCUS BM562913 1016 bp mRNA linear EST 20-FEB-2002
DEFINITION AGENCOURT_6566679 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5736771
5', mRNA sequence.
ACCESSION BM562913
VERSION BM562913.1 GI:18809393
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 1016)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Straubeberg, Ph.D.
Email: cgabps@mail.nih.gov
Tissue Procurement: ARCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12745 row: n column: 04
High quality sequence stop: 637.
Location/Qualifiers
1..1016
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5736771"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_88"
/notes="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.0346 Length: 1016
Score: 82.00 Matches: 19
Percent Similarity: 79.50% Conservatives: 2
Best Local Similarity: 79.17% Mismatches: 1
Query Match: 62.12% Indels: 2
DB: 3 Gaps: 0

US-09-632-036F-6 (1-24) x BM562913 (1-1016)

Qy 1 ProLeuHisAenGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCys 20
Db 797 CCCCTGCACACCAAGAGGTGACCGCAGAGATGGAACACACACCGCGTGTGAAAAAGTGCA 856
Qy 20 erLysPro 22
Db 1 Gaps: 0

```

Db	857	ACCAGCCC	864	
RESULT 35				
AI908047/c				
LOCUS	AI908047	115 bp	mRNA	linear EST 30-MAR-2000
DEFINITION	QV-BT161-220499-124	BT161	Homo sapiens	cDNA, mRNA sequence.
ACCESSION	AI908047			
VERSION	AI908047.1	GI:6498727		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	1 (bases 1 to 115)			
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)		3491-3496 (2000)
PUBMED	10737800			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT161-124.html&t3=220499&t4=1) Seq primer: puc 18 forward.			
FEATURES	Location/Qualifiers			
source	1..115			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/sex="female"			
	/dev_stage="Adult"			
	/clone_lib="BT161"			
	/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
ORIGIN				
Alignment Scores:				
Pred. No.:	0.0345	Length:	115	
Score:	75.00	Matches:	13	
Percent Similarity:	92.86%	Conservative:	0	
Best Local Similarity:	92.86%	Mismatches:	1	
Query Match:	56.82%	Indels:	0	
DB:	1	Gaps:	0	
US-09-632-036F-6 (1-24) x AI908047 (1-115)				
QY	11	AspGlyThrGlnArgAlaGluLysCysSerLysProCysAla	24	
Db	113	GATGGAACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCC	72	
RESULT 36				
BG954969/c				
LOCUS	BG954969	266 bp	mRNA	linear EST 12-JUN-2001
DEFINITION	CM4-CT0656-120201-854-f06	CT0656	Homo sapiens	cDNA, mRNA sequence.

ACCESSION	BG954969			
VERSION	BG954969.1	GI:14373140		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE				
AUTHORS	1 (bases 1 to 266)			
	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.			
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	97 (7)		3491-3496 (2000)
PUBMED	10737800			
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CT0656-120201-854-f06&t3=2001-02-12&t4=1) Seq primer: puc 18 forward High quality sequence start: 11 High quality sequence stop: 266.			
FEATURES	Location/Qualifiers			
source	1..266			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/dev_stage="Adult"			
	/clone_lib="CT0656"			
	/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."			
ORIGIN				
Alignment Scores:				
Pred. No.:	7.34	Length:	266	
Score:	63.00	Matches:	11	
Percent Similarity:	91.67%	Conservative:	0	
Best Local Similarity:	91.67%	Mismatches:	1	
Query Match:	47.73%	Indels:	0	
DB:	2	Gaps:	0	
US-09-632-036F-6 (1-24) x BG954969 (1-266)				
QY	13	ThrGlnArgAlaGluLysCysSerLysProCysAla	24	
Db	264	ACACAGCGGTGTGAGAGTGCAGCAAGCCCTGTGCC	229	
RESULT 37				
BX336780				
LOCUS	BX336780	709 bp	mRNA	linear EST 08-APR-2004
DEFINITION	BX336780	Homo sapiens	PLACENTA COT 25-NORMALIZED	Homo sapiens cDNA clone CSODI032YB05 5-PRIME, mRNA sequence.
ACCESSION	BX336780			
VERSION	BX336780.2	GI:46282048		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
1 (bases 1 to 709)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30345544.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
8568.f

FEATURES

source
Location/Qualifiers
1..709
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1032YB05"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Alignment Scores:
Pred. No.: 23.2 Length: 709
Score: 63.00 Matches: 12
Percent Similarity: 68.18% Conservative: 3
Best Local Similarity: 54.55% Mismatches: 7
Query Match: 47.73% Indels: 0
DB: 5 Gaps: 0

US-09-632-036F-6 (1-24).x BX336780 (1-709)

Qy 2 LeuHisAsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLys 21
Db 202 CTGTACAACCAAGAGTGATCATCGATGATGTWACAYGGTGTGAGWATTGTAGYWAG 261

Qy 22 ProCys 23
Db 262 CVCTGT 267

RESULT 38
CW538167/c
LOCUS
DEFINITION
Oryza punctata
3' genomic survey sequence.
ACCESSION CW538167 GI:54012389
VERSION CW538167.1
KEYWORDS GSS.
SOURCE Oryza punctata
ORGANISM Oryza punctata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
1 (bases 1 to 708)
SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wissotski, M., Yost, D.,
Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,
Hatfield, J., Soderlund, C., Wing, R. and Jackson, S.A.
OMAP Project - Purdue University
Unpublished (2004)
Contact: Scott A. Jackson

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS

Qy 4 AsnGlnGluValThrAlaGluAspGlyThrGlnArgAlaGluLysCysSerLysProCys 23
Db 304 GATGAGGAAGTCAGTAAGAGGAGGATCCACCAGACTGCTGTTCTGCACCTTGT 245

Qy 24 Ala 24
Db 244 GCA 242

RESULT 39
CNS06U0A
LOCUS
DEFINITION
T7 end of clone AX0AA003H07 of library AX0AA from strain CBS 7064
of Pichia farinosa, genomic survey sequence.
ACCESSION AL415232 GI:12194198
VERSION AL415232.1
KEYWORDS GSS.
SOURCE Pichia farinosa
ORGANISM Pichia farinosa
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
1 (bases 1 to 1004)
Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G.,
Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertuy, A., Neuvéglise, C., Olier-Kalogeropoulos, O., Potier, S.,
Saurin, W., Tekaija, F., Toffano-Nioche, C., Wesolowski-Louvel, M.,
Wincker, P. and Weissenbach, J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
1152876
2 (bases 1 to 1004)
de Montigny, J., Spohnner, C., Souciet, J., Tekaija, F., Dujon, B.,
Wincker, P., Artiguenave, F. and Potier, S.

ORIGIN	Alignment Scores:	Length:	552
	Pred. No.:	Matches:	13
	Score:		

Score:	62.38	Matches:	13
Percent Similarity:	66.67%	Conservative:	1
Best Local Similarity:	61.90%	Mismatches:	6
Query Match:	46.59%	Indels:	1
DB:	9	Gaps:	1
US-09-632-036F-6 (1-24) x BH011016 (1-552)			

Db	66	ATCCATAACGGTTTCTAGTACAGTTCAAGATGGGACTCAAAACAGCAGCAAAATGT	122
Qy	22	Pro	22
Db	123	CCT	125



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:34:18 ; Search time 125.455 Seconds
(without alignments)
70.046 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSHCVLDLDDKCPAEQR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: Genesecp1980s.*
- 2: Genesecp1990s.*
- 3: Genesecp2000s.*
- 4: Genesecp2001s.*
- 5: Genesecp2002s.*
- 6: Genesecp2003as.*
- 7: Genesecp2003bs.*
- 8: Genesecp2004s.*
- 9: Genesecp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	100.0	22	4	AB686633
2	105	92.1	30	6	ABJ18655
3	105	92.1	30	6	ABP59259
4	105	92.1	42	3	ABY84783
5	105	92.1	42	3	ABY84784
6	105	92.1	69	2	AAW53132
7	105	92.1	149	6	ABJ18657
8	105	92.1	149	6	ABP59261
9	105	92.1	435	8	ADP10480
10	105	92.1	470	9	ADY30515
11	105	92.1	493	7	ADG17936
12	105	92.1	653	3	ABAB21200
13	105	92.1	653	5	AAW51145
14	105	92.1	675	9	ADW87401
15	105	92.1	678	8	ADT50884
16	105	92.1	678	9	ADZ47795
17	105	92.1	680	9	ADY28115
18	105	92.1	680	7	ADG17945
19	105	92.1	696	9	ADW28504
20	105	92.1	712	3	ABAB21204
21	105	92.1	712	5	AAW51149
22	105	92.1	715	7	ADG17944
23	105	92.1	717	9	ADZ47807
24	105	92.1	720	7	ADG17940

25	105	92.1	741	7	ADM29356
26	105	92.1	782	2	AAW19764
27	105	92.1	815	8	ADT50879
28	105	92.1	835	9	ADY30511
29	105	92.1	879	9	ADY30514
30	105	92.1	919	3	ABAB21203
31	105	92.1	919	5	AAW51148
32	105	92.1	951	3	AAV44993
33	105	92.1	960	9	ADY30513
34	105	92.1	970	9	ADY30509
35	105	92.1	1042	7	ADM29352
36	105	92.1	1200	3	ABAB21208
37	105	92.1	1217	8	ADT50876
38	105	92.1	1223	5	AAU98923
39	105	92.1	1253	7	ADC35106
40	105	92.1	1255	2	AAW01111
41	105	92.1	1255	2	AAW92406
42	105	92.1	1255	3	AAV92620
43	105	92.1	1255	3	AAV84780
44	105	92.1	1255	3	ABAB21198
45	105	92.1	1255	4	ABAB60167
46	105	92.1	1255	4	ABG88267
47	105	92.1	1255	4	AAE12130
48	105	92.1	1255	4	AAAB85458
49	105	92.1	1255	5	AAE20479
50	105	92.1	1255	5	AAU77114
51	105	92.1	1255	5	AAE26349
52	105	92.1	1255	5	AAE26366
53	105	92.1	1255	5	AAU74545
54	105	92.1	1255	5	AAW51143
55	105	92.1	1255	5	AAE24067
56	105	92.1	1255	6	ABR47447
57	105	92.1	1255	6	ABP74708
58	105	92.1	1255	6	ABR43687
59	105	92.1	1255	6	AAE38390
60	105	92.1	1255	6	ADA38143
61	105	92.1	1255	7	ABR82066
62	105	92.1	1255	7	ABR82066
63	105	92.1	1255	7	ABR67621
64	105	92.1	1255	7	ADC09593
65	105	92.1	1255	7	ADZ5484
66	105	92.1	1255	7	ADZ5484
67	105	92.1	1255	7	ADZ5484
68	105	92.1	1255	7	ADZ5484
69	105	92.1	1255	8	ADH13187
70	105	92.1	1255	8	ADJ66554
71	105	92.1	1255	8	ADM12582
72	105	92.1	1255	8	ADM72831
73	105	92.1	1255	8	ADL90083
74	105	92.1	1255	8	ADQ38813
75	105	92.1	1255	8	ADQ20009
76	105	92.1	1255	8	ADQ17193
77	105	92.1	1255	8	ADQ29700
78	105	92.1	1255	8	ADQ75930
79	105	92.1	1255	8	ADQ75930
80	105	92.1	1255	8	ADQ75930
81	105	92.1	1255	8	ABM81864
82	105	92.1	1255	8	ADP80108
83	105	92.1	1255	8	ADU04314
84	105	92.1	1255	9	ADW44355
85	105	92.1	1255	9	ADW95472
86	105	92.1	1255	9	ADW28640
87	105	92.1	1255	9	ADW87390
88	105	92.1	1255	9	ADZ28137
89	105	92.1	1255	9	ADZ47863
90	105	92.1	1255	9	ADZ09807
91	105	92.1	1255	9	ADZ72380
92	105	92.1	1255	9	AEA15074
93	105	92.1	1255	9	AEA08355
94	105	92.1	1255	9	ABE87742
95	105	92.1	1255	9	ADZ47803
96	105	92.1	1255	9	ADY30508
97	105	92.1	1255	9	ADY30512
98	105	92.1	1255	9	ADY30512
99	105	92.1	1255	9	ADY30512
100	105	92.1	1255	9	ADY30512

98 105 92.1 1414 9 ADY30510 Human spl
99 105 92.1 1433 2 AAR39568 Sequence
100 100 87.7 1255 8 ADQ75969 Rhesus mo

ALIGNMENTS

RESULT 1
AAB68633
ID AAB68633 standard; peptide; 22 AA.
XX
AC AAB68633;
XX
DT 30-APR-2001 (first entry)
XX
DE HER-2 B cell epitope #12.
XX
KW Cytostatic; immune response; HER-2; human; epitope; cancer; breast;
KW ovarian; lung; prostate; colon.
XX
OS Homo sapiens.
XX
FN WO200108636-A2.
XX
PD 08-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-US021222.
XX
XX 03-AUG-1999; 99US-0146869P.
XX
PA (OHIS) UNIV OHIO STATE.
XX
PI Kaumaya PT, Stevens VC, Triozzi PL;
XX
DR WPI; 2001-182849/18.
XX
PT Compositions comprising polypeptides and polynucleotides for stimulating
PT the immune system and for treating malignancies associated with
PT overexpression of the HER-2 protein.
XX
XX Claim 1; Page 37; 51pp; English.

XX The present invention relates to compositions for stimulating the immune
CC system and for treating malignancies associated with overexpression of
CC the HER-2 protein. The compositions comprise immunogenic groups of the
CC HER-2 proteins. The present sequence is one such peptide used in the
CC compositions of the present invention. The compositions can be used for
CC treating cancer, e.g. breast, ovarian, lung, prostate and colon cancers
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 114; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 INGTSCVDLDDKGCPEQR 20
|||
DB 1 INGTSCVDLDDKGCPEQR 20

RESULT 2
ABJ18655
ID ABJ18655 standard; peptide; 30 AA.
XX
AC ABJ18655;
XX
DT 20-FEB-2003 (first entry)
XX
DE ErbB receptor antagonist peptide #38.
XX
KW Vaccine; erbB receptor antagonist; tumour; cancer; gastric cancer;
KW breast cancer; prostate cancer.

XX Unidentified.
OS
FN WO200281649-A2.
XX
PD 17-OCT-2002.
XX
PF 08-APR-2002; 2002WO-US011211.
XX
PR 06-APR-2001; 2001US-0282037P.
PR 03-AUG-2001; 2001US-0309864P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Zhang H, Murali R, Richter M, Berezov A, Liu Q;
PI Chen J;
XX
DR WPI; 2003-075482/07.
XX
PT New peptide antagonists against erbB receptors, useful for preventing or
PT treating tumors or cancers (e.g. lung adenocarcinomas, breast carcinomas
PT or prostate cancer) in humans.
XX
PS Disclosure; Page 22; 115pp; English.
XX
CC The invention comprises peptide antagonists designed to target erbB
CC receptors. The erbB receptor peptide antagonists are useful for
CC preventing tumours and cancers (e.g. gastric cancer, breast cancer and
CC prostate cancer). The present amino acid sequence represents an erbB
CC receptor peptide antagonist of the invention
XX
SQ Sequence 30 AA;

Query Match 92.1%; Score 105; DB 6; Length 30;
Best Local Similarity 95.0%; Pred. No. 1.8e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTSCVDLDDKGCPEQR 20
|||
DB 4 INGTSCVDLDDKGCPEQR 23

RESULT 3
ABP59259
ID ABP59259 standard; peptide; 30 AA.
XX
AC ABP59259;
XX
DT 10-MAY-2003 (first entry)
XX
DE Peptide epitope for generating cell surface receptor antibody, SEQ ID 38.
XX
KW Antibody; cytostatic; vaccine; cell surface receptor; erbB; TNF;
KW immunoglobulin gene superfamily; IGSF; epitope.
XX
OS Synthetic.
XX
FN WO2003012072-A2.
XX
PD 13-FEB-2003.
XX
PF 05-AUG-2002; 2002WO-US024892.
XX
PR 03-AUG-2001; 2001US-0309864P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Greene MI, Zhang H, Richter M, Murali R;
XX
DR WPI; 2003-268117/26.
XX
PT Novel antibody for preventing, treating, imaging or diagnosing tumor, has
PT specificity for activated cell surface receptor and binds specifically to

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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:35:58 ; Search time 29.5455 Seconds
(without alignments)
55.965 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVLDLDDKCPAEQR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

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4: /cgn2_6/prodata/1/iaa/ECTUS COMB.pep.*

5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	105	92.1	782	1	US-09-146-283-4
2	105	92.1	782	2	US-08-579-823A-4
3	105	92.1	782	2	US-09-344-195-4
4	105	92.1	1255	1	US-08-467-083-68
5	105	92.1	1255	1	US-08-414-417B-68
6	105	92.1	1255	1	US-08-484-438-8
7	105	92.1	1255	1	US-08-486-348A-68
8	105	92.1	1255	1	US-08-625-101-2
9	105	92.1	1255	1	US-08-468-545B-68
10	105	92.1	1255	1	US-08-356-786-2
11	105	92.1	1255	2	US-08-466-680B-68
12	105	92.1	1255	2	US-09-811-487-2
13	105	92.1	1255	2	US-09-811-115-3
14	105	92.1	1255	2	US-09-354-533-68
15	105	92.1	1255	2	US-09-441-411-6
16	105	92.1	1255	2	US-09-167-516-2
17	95	83.3	624	2	US-08-422-108-1
18	95	83.3	624	2	US-08-422-734-1
19	95	83.3	645	2	US-09-602-812A-13
20	50	43.9	122	2	US-09-732-210-241
21	50	43.9	122	2	US-09-732-210-585
22	50	43.9	125	2	US-09-438-185A-639
23	47	41.2	274	2	US-09-188-930-336
24	47	41.2	274	2	US-09-312-283C-336
25	47	41.2	439	2	US-09-409-096-6
26	47	41.2	443	1	US-08-833-963C-2
27	47	41.2	443	2	US-08-980-514-1
28	47	41.2	47	28	US-09-949-016-7792
29	45	39.5	116	2	US-09-270-767-57685
30	45	39.5	124	2	US-09-270-767-31669
31	45	39.5	124	2	US-09-270-767-46886
32	45	39.5	203	2	US-09-248-796A-15633
33	45	39.5	342	2	US-09-902-540-15847
34	44	38.6	334	2	US-09-800-729-109
35	44	38.6	780	2	US-09-248-796A-16702
36	44	38.6	1060	2	US-09-248-796A-14123
37	43	37.7	324	1	US-08-484-993B-22
38	43	37.7	324	1	US-08-484-158B-22
39	43	37.7	324	1	US-08-484-596A-22
40	43	37.7	324	1	US-08-480-150A-22
41	43	37.7	324	2	US-08-458-731-22
42	43	37.7	324	2	US-08-149-223A-22
43	43	37.7	416	2	US-09-538-092-392
44	43	37.7	585	2	US-09-270-767-59685
45	43	37.7	621	2	US-09-489-039A-10378
46	43	37.7	801	2	US-09-270-767-44264
47	42.5	37.3	201	2	US-09-710-279-1514
48	42.5	37.3	255	2	US-09-134-001C-3498
49	42	36.8	90	2	US-09-248-796A-19142
50	42	36.8	101	2	US-09-716-129-80
51	42	36.8	132	2	US-09-716-129-179
52	42	36.8	321	2	US-09-270-767-33762
53	42	36.8	321	2	US-09-270-767-48979
54	42	36.8	324	2	US-09-605-703B-1888
55	42	36.8	1390	2	US-09-902-540-11251
56	42	36.8	2813	2	US-08-896-449A-2
57	42	36.8	2813	2	US-09-132-652-2
58	42	36.8	2813	2	US-09-886-900A-2
59	42	36.8	2813	2	US-09-662-478C-2
60	42	36.8	3457	1	US-08-416-603-4
61	41	36.0	136	2	US-09-252-991A-16772
62	41	36.0	864	1	US-08-209-521-29
63	41	36.0	864	2	US-09-265-503B-138
64	40.5	35.5	497	2	US-09-252-991A-31534
65	40.5	35.5	726	6	5208144-37
66	40	35.1	120	2	US-09-248-796A-19679
67	40	35.1	124	2	US-09-513-999C-4218
68	40	35.1	214	2	US-09-902-540-16784
69	40	35.1	232	2	US-09-248-796A-14122
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71	40	35.1	246	2	US-09-248-796A-18240
72	40	35.1	265	2	US-09-252-991A-24304
73	40	35.1	303	6	5340934-13
74	40	35.1	317	2	US-09-270-767-43541
75	40	35.1	368	2	US-09-668-097A-38
76	40	35.1	551	2	US-09-252-991A-26416
77	39.5	34.6	194	2	US-08-679-493A-215
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79	39.5	34.6	357	2	US-09-645-168-3
80	39.5	34.6	1172	1	US-08-313-288B-19
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83	39.5	34.6	4654	2	US-08-476-515A-84
84	39.5	34.6	4655	2	US-08-652-877-84
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87	39.5	34.6	4655	2	US-08-652-877-90
88	39.5	34.6	5405	2	US-08-718-388-9
89	39	34.2	187	2	US-08-463-682-1
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91	39	34.2	220	2	US-08-463-682-24
92	39	34.2	226	1	US-08-463-682-23
93	39	34.2	225	2	US-08-347-594A-4
94	39	34.2	227	2	US-09-252-991A-24444
95	39	34.2	229	2	US-09-248-796A-16698
96	39	34.2	230	2	US-09-902-540-15990
97	39	34.2	240	2	US-09-461-912A-41
98	39	34.2	247	1	US-08-797-689-4
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100	39	34.2	257	2	US-09-949-016-11037

ALIGNMENTS

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RESULT 1
US-09-146-283-4
; Sequence 4, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
US-09-146-283-4
Query Match 92.1%; Score 105; DB 1; Length 782;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTHSCVDLDDKGCPEQR 20
Db 628 INCTHSCVDLDDKGCPEQR 647

RESULT 2
US-08-579-823A-4
; Sequence 4, Application US/08579823A
; Patent No. 6080409
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Composition and Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
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; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,823A
; FILING DATE: 03-DEC-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 782 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-Her-2 fusion protein; Fig. 8
US-08-579-823A-4
Query Match 92.1%; Score 105; DB 2; Length 782;
Best Local Similarity 95.0%; Pred. No. 1.2e-07;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTHSCVDLDDKGCPEQR 20
Db 628 INCTHSCVDLDDKGCPEQR 647

RESULT 3
US-09-344-195-4
; Sequence 4, Application US/09344195
; Patent No. 6210662
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/344,195
; FILING DATE: 24-Jun-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
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Title: US-09-632-036F-42

Perfect score: 114

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published Applications_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	92.1	493	4	US-10-412-804A-2
2	105	92.1	653	3	US-09-854-356-3
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4	105	92.1	680	5	US-10-846-113A-5
5	105	92.1	690	4	US-10-412-804A-11
6	105	92.1	712	3	US-09-854-356-7
7	105	92.1	715	4	US-10-412-804A-10
8	105	92.1	717	5	US-10-956-373-14
9	105	92.1	720	4	US-10-412-804A-6
10	105	92.1	919	3	US-09-854-356-6
11	105	92.1	1253	4	US-10-146-473-72
12	105	92.1	1255	3	US-09-811-123-9
13	105	92.1	1255	3	US-09-811-115-3
14	105	92.1	1255	3	US-09-765-973-2
15	105	92.1	1255	3	US-09-354-533-68
16	105	92.1	1255	3	US-09-769-508-2
17	105	92.1	1255	3	US-09-854-356-1
18	105	92.1	1255	3	US-09-930-125-2
19	105	92.1	1255	3	US-09-441-411-6
20	105	92.1	1255	3	US-09-984-092-4
21	105	92.1	1255	4	US-10-207-655-45
22	105	92.1	1255	4	US-10-177-293-126
23	105	92.1	1255	4	US-10-207-498-6
24	105	92.1	1255	4	US-10-338-730-2
25	105	92.1	1255	4	US-10-313-644-2
26	105	92.1	1255	4	US-10-322-892-4
27	105	92.1	1255	4	US-10-272-437A-28

28	105	92.1	1355	4	US-10-117-937-594	Sequence 594, App
29	105	92.1	1355	4	US-10-418-027-3	Sequence 3, Appli
30	105	92.1	1355	4	US-10-394-322A-17	Sequence 17, Appl
31	105	92.1	1355	4	US-10-245-871-553	Sequence 553, App
32	105	92.1	1355	4	US-10-435-696-36	Sequence 36, Appl
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35	105	92.1	1355	4	US-10-253-286-553	Sequence 553, App
36	105	92.1	1355	4	US-10-147-005-68	Sequence 68, Appl
37	105	92.1	1355	4	US-10-149-138-4641	Sequence 4641, Ap
38	105	92.1	1355	4	US-10-441-779C-4	Sequence 4, Appli
39	105	92.1	1355	4	US-10-734-564-126	Sequence 126, App
40	105	92.1	1355	4	US-10-657-022-90	Sequence 90, Appl
41	105	92.1	1355	5	US-10-762-128-6	Sequence 6, Appli
42	105	92.1	1355	5	US-10-484-108-1	Sequence 1, Appli
43	105	92.1	1355	5	US-10-723-860-9	Sequence 9, Appli
44	105	92.1	1355	5	US-10-615-343-17	Sequence 17, Appl
45	105	92.1	1355	5	US-10-794-514A-1	Sequence 1, Appli
46	105	92.1	1355	5	US-10-871-708-9	Sequence 9, Appli
47	105	92.1	1355	5	US-10-983-340-17	Sequence 17, Appl
48	105	92.1	1355	5	US-10-846-113A-27	Sequence 27, Appl
49	105	92.1	1355	6	US-11-067-064-594	Sequence 594, App
50	105	92.1	1355	6	US-11-121-347-68	Sequence 68, Appl
51	105	92.1	1355	6	US-11-037-713-12	Sequence 12, Appl
52	105	92.1	1355	6	US-11-067-159-594	Sequence 594, App
53	105	92.1	1394	5	US-10-956-373-10	Sequence 10, Appl
54	98	86.0	177	5	US-10-949-667-5	Sequence 5, Appli
55	98	86.0	654	3	US-09-854-356-8	Sequence 8, Appli
56	98	86.0	1256	3	US-09-854-356-2	Sequence 2, Appli
57	98	86.0	1256	3	US-09-854-356-14	Sequence 14, Appl
58	98	86.0	1257	5	US-10-484-067-2	Sequence 2, Appli
59	98	86.0	1260	3	US-09-870-759-118	Sequence 118, App
60	98	86.0	1260	3	US-09-751-708A-118	Sequence 118, App
61	98	86.0	1260	4	US-10-428-817A-114	Sequence 114, App
62	98	86.0	1260	5	US-10-937-758A-95	Sequence 95, Appl
63	98	86.0	1260	5	US-10-949-667-8	Sequence 8, Appli
64	95	83.3	645	4	US-09-921-161-1	Sequence 1, Appli
65	95	83.3	645	4	US-10-268-501-13	Sequence 13, Appl
66	95	83.3	645	4	US-10-608-626-13	Sequence 13, Appl
67	95	83.3	645	5	US-10-719-310-13	Sequence 13, Appl
68	95	83.3	645	5	US-11-044-749-13	Sequence 13, Appl
69	95	83.3	645	6	US-11-154-465-13	Sequence 13, Appl
70	88	77.2	15	4	US-10-149-138-3948	Sequence 3948, Ap
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75	82	71.9	275	5	US-10-484-067-10	Sequence 10, Appl
76	81	71.1	15	4	US-10-149-138-3734	Sequence 3734, Ap
77	81	71.1	15	4	US-10-149-138-3734	Sequence 3734, Ap
78	81	71.1	16	3	US-09-811-123-11	Sequence 11, Appl
79	81	71.1	50	5	US-10-484-067-11	Sequence 11, Appl
80	78	68.4	50	5	US-10-484-067-5	Sequence 5, Appli
81	78	68.4	275	5	US-10-484-067-4	Sequence 4, Appli
82	66	57.9	11	4	US-10-149-138-194	Sequence 194, App
83	66	57.9	11	4	US-10-149-138-2511	Sequence 2511, Ap
84	66	57.9	11	4	US-10-149-138-194	Sequence 194, App
85	66	57.9	11	4	US-10-149-138-2511	Sequence 2511, Ap
86	62	54.4	11	4	US-10-149-138-2798	Sequence 2798, Ap
87	62	54.4	11	4	US-10-149-138-3404	Sequence 3404, Ap
88	62	54.4	11	4	US-10-149-138-2798	Sequence 2798, Ap
89	62	54.4	11	4	US-10-149-138-3404	Sequence 3404, Ap
90	59	51.8	15	4	US-10-149-138-3841	Sequence 3841, Ap
91	59	51.8	15	4	US-10-149-138-3841	Sequence 3841, Ap
92	58	50.9	10	4	US-10-149-138-2521	Sequence 2521, Ap
93	58	50.9	10	4	US-10-149-138-3233	Sequence 3233, Ap
94	58	50.9	10	4	US-10-149-138-3233	Sequence 3233, Ap
95	58	50.9	10	4	US-10-149-138-3233	Sequence 3233, Ap
96	58	50.9	11	4	US-10-149-138-2522	Sequence 2522, Ap
97	58	50.9	11	4	US-10-149-138-2522	Sequence 2522, Ap
98	57	50.0	10	4	US-10-149-138-3106	Sequence 3106, Ap
99	57	50.0	10	4	US-10-149-138-3106	Sequence 3106, Ap
100	57	50.0	11	4	US-10-149-138-859	Sequence 859, App

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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:48:55 ; Search time 5.90909 Seconds
(without alignments)
16.207 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVDLDKGPFAEQR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA_New.*

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3: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*

4: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*

5: /cgn2_6/ptodata1/pubpaa/PCT_NEW_PUB.pep.*

6: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*

7: /cgn2_6/ptodata1/pubpaa/US11_NEW_PUB.pep.*

8: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	105	92.1	US-11-022-562-213	Sequence 213, App
2	47	41.2	US-10-131-826A-318	Sequence 318, App
3	42.5	37.3	US-10-793-626-1514	Sequence 1514, App
4	39.5	34.6	US-10-485-517-167	Sequence 167, App
5	39.5	34.6	US-11-108-172-1116	Sequence 1116, App
6	39	34.2	US-10-821-234-1133	Sequence 1133, App
7	38.5	33.8	US-10-821-234-1412	Sequence 1412, App
8	38	33.3	US-10-821-234-1216	Sequence 1216, App
9	38	33.3	US-10-131-826A-296	Sequence 296, App
10	38	33.3	US-10-467-657-7260	Sequence 7260, App
11	38	33.3	US-10-858-730-59	Sequence 59, App
12	38	33.3	US-11-067-811-1	Sequence 1, Appli
13	38	33.3	US-11-067-811-4	Sequence 4, Appli
14	37.5	32.9	US-10-131-826A-290	Sequence 290, App
15	37.5	32.9	US-11-074-176-96	Sequence 96, Appl
16	37	32.5	US-11-065-669-5	Sequence 5, Appli
17	37	32.5	US-11-051-568-29	Sequence 29, Appl
18	37	32.5	US-11-137-465-47	Sequence 47, Appl
19	37	32.5	US-10-420-192-6	Sequence 6, Appli
20	36.5	32.0	US-10-821-234-1093	Sequence 1093, App
21	36.5	32.0	US-11-108-528-82	Sequence 82, Appl
22	36.5	32.0	US-10-821-234-916	Sequence 916, App
23	36	31.6	US-10-467-657-7616	Sequence 7616, App
24	36	31.6	US-10-624-932-2	Sequence 2, Appli
25	36	31.6	US-11-108-172-1095	Sequence 1095, App

26	35.5	31.1	US-10-821-234-975	Sequence 975, App
27	35.5	31.1	US-11-113-424-37	Sequence 37, Appl
28	35	30.7	US-10-467-657-3166	Sequence 3166, App
29	35	30.7	US-10-485-517-361	Sequence 361, App
30	35	30.7	US-11-113-424-79	Sequence 79, Appl
31	35	30.7	US-10-131-826A-432	Sequence 432, App
32	35	30.7	US-10-967-457-77	Sequence 77, Appl
33	35	30.7	US-10-821-234-1376	Sequence 1376, App
34	35	30.7	US-11-021-441-35	Sequence 35, Appl
35	35	30.7	US-10-645-441-15	Sequence 15, Appl
36	35	30.7	US-10-821-234-1303	Sequence 1303, App
37	34.5	30.3	US-11-113-424-38	Sequence 38, Appl
38	34.5	30.3	US-11-137-465-57	Sequence 57, Appl
39	34.5	30.3	US-10-508-263-96	Sequence 96, Appl
40	34.5	30.3	US-11-137-465-35	Sequence 35, Appl
41	34.5	30.3	US-11-113-424-35	Sequence 35, Appl
42	34.5	30.3	US-11-137-465-58	Sequence 58, Appl
43	34.5	30.3	US-11-113-424-2	Sequence 2, Appli
44	34.5	30.3	US-11-147-047-51	Sequence 51, Appl
45	34.5	30.3	US-11-137-465-36	Sequence 36, Appl
46	34.5	30.3	US-11-113-424-36	Sequence 36, Appl
47	34	29.8	US-10-821-234-1236	Sequence 1236, App
48	34	29.8	US-10-793-626-3170	Sequence 3170, App
49	34	29.8	US-10-967-527A-27	Sequence 27, Appl
50	34	29.8	US-10-821-234-1502	Sequence 1502, App
51	34	29.8	US-10-467-657-9211	Sequence 9211, App
52	34	29.8	US-10-793-626-2052	Sequence 2052, App
53	34	29.8	US-11-113-424-53	Sequence 53, Appl
54	33.5	29.4	US-11-177-010-2	Sequence 2, Appli
55	33.5	29.4	US-11-177-010-4	Sequence 4, Appli
56	33.5	29.4	US-11-055-822-908	Sequence 908, App
57	33.5	29.4	US-10-821-234-1556	Sequence 1556, App
58	33.5	29.4	US-11-108-528-80	Sequence 80, Appl
59	33.5	29.4	US-11-108-172-1068	Sequence 1068, App
60	33	28.9	US-10-467-657-7022	Sequence 7022, App
61	33	28.9	US-10-467-657-3792	Sequence 3792, App
62	33	28.9	US-10-467-657-1360	Sequence 1360, App
63	33	28.9	US-10-467-657-2884	Sequence 2884, App
64	33	28.9	US-11-055-822-210	Sequence 210, App
65	33	28.9	US-11-055-822-726	Sequence 726, App
66	33	28.9	US-10-467-657-3894	Sequence 3894, App
67	33	28.9	US-10-467-657-7242	Sequence 7242, App
68	33	28.9	US-10-793-626-3168	Sequence 3168, App
69	33	28.9	US-10-793-626-2034	Sequence 2034, App
70	33	28.9	US-11-012-762-42	Sequence 42, Appl
71	33	28.9	US-11-102-240-22	Sequence 22, Appl
72	33	28.9	US-10-793-626-1386	Sequence 1386, App
73	33	28.9	US-11-191-374-4	Sequence 4, Appli
74	33	28.9	US-11-191-375-4	Sequence 4, Appli
75	33	28.9	US-11-113-837-21	Sequence 21, Appl
76	33	28.9	US-11-102-240-16	Sequence 16, Appl
77	33	28.9	US-10-821-234-1314	Sequence 1314, App
78	33	28.9	US-11-081-566-2	Sequence 2, Appli
79	33	28.9	US-11-108-172-1122	Sequence 122, App
80	33	28.9	US-11-082-389-362	Sequence 362, App
81	33	28.9	US-10-510-386-10	Sequence 10, Appl
82	33	28.9	US-11-191-375-18	Sequence 18, Appl
83	33	28.9	US-11-191-375-18	Sequence 18, Appl
84	33	28.9	US-11-191-374-46	Sequence 46, Appl
85	33	28.9	US-11-191-375-46	Sequence 46, Appl
86	33	28.9	US-10-131-826A-464	Sequence 464, App
87	33	28.9	US-10-467-657-854	Sequence 854, App
88	33	28.9	US-11-113-424-39	Sequence 39, Appl
89	33	28.9	US-11-091-668-2	Sequence 2, Appli
90	33	28.9	US-11-191-374-10	Sequence 10, Appl
91	33	28.9	US-11-191-375-10	Sequence 10, Appl
92	33	28.9	US-10-858-730-222	Sequence 222, App
93	33	28.9	US-11-091-668-4	Sequence 4, Appli
94	33	28.9	US-10-821-234-1045	Sequence 1045, App
95	32.5	28.5	US-10-793-626-158	Sequence 158, App
96	32.5	28.5	US-11-085-775-4	Sequence 4, Appli
97	32.5	28.5	US-10-467-657-3082	Sequence 3082, App
98	32.5	28.5	US-11-018-018-1	Sequence 1, Appli

Sequence 1, Appli
Sequence 84, Appli

99 32.5 28.5 747 7 US-11-047-757-1
100 32.5 28.5 1613 7 US-11-108-528-84

ALIGNMENTS

RESULT 1
US-11-022-562-213
; Sequence 213, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-022-562-213

Query Match 92.1%; Score 105; DB 7; Length 1255;
Best Local Similarity 95.0%; Pred. No. 1,1e-09;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTSCVDLDDKGPAPQR 20
DB 628 INGTSCVDLDDKGPAPQR 647

RESULT 2
US-10-131-826A-318
; Sequence 318, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RJC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 318
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-318

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Best Local Similarity 58.8%; Pred. No. 0.85;
Matches 10; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY 6 SCVDLDDKGPAPQR 20
DB 200 SCVDNCECDMGAPCEQR 216

RESULT 3
US-10-793-626-1514
; Sequence 1514, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1514
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1514

Query Match 37.3%; Score 42.5; DB 6; Length 201;
Best Local Similarity 43.5%; Pred. No. 2.1;
Matches 10; Conservative 2; Mismatches 6; Indels 5; Gaps 2;
QY 2 NGTSCVDLDDKGC---PAEQR 20
DB 48 NGVHTCID-TSAGCVNDTPAFNR 69

RESULT 4
US-10-485-517-167
; Sequence 167, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides

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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:36:13 ; Search time 20.9091 Seconds
(without alignments)
92.033 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSHCVLDLDKGCPEQR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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PIR_80:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	92.1	1255	1 A24571	protein-tyrosine k
2	98	86.0	1254	2 I48161	p-185 precursor -
3	98	86.0	1260	1 TVRNU	protein-tyrosine k
4	51	44.7	235	2 S30001	ribosomal protein
5	50	43.9	122	2 B86570	L14 ribosomal prot
6	50	43.9	122	2 G72054	ribosomal protein
7	50	43.9	122	2 E81664	ribosomal protein
8	50	43.9	122	2 D42645	ribosomal protein
9	49	43.0	303	2 A84344	NADH dehydrogenase
10	47	41.2	1435	2 S54697	DNA polymerase III
11	47	41.2	1435	2 C90596	hypothetical prote
12	46.5	40.8	548	2 T16642	hypothetical prote
13	46	40.4	462	1 A37986	interleukin-6 rece
14	45	39.5	111	2 T36163	probable transcrip
15	45	39.5	140	2 C90850	conserved hypotet
16	44	38.6	124	2 G87028	hypothetical prote
17	44	38.6	129	2 AE0206	conserved hypotet
18	44	38.6	542	2 B90090	very similar to mo
19	44	38.6	747	2 T23042	hypothetical prote
20	44	38.6	749	2 T23045	hypothetical prote
21	44	38.6	1419	2 T20531	agglutinin-like ad
22	44	38.6	2643	2 T29141	hypothetical prote
23	43.5	38.2	4660	2 T42737	gp330 protein prec
24	43	37.7	304	2 G85068	N7-like protein [i
25	43	37.7	416	2 S48957	hypothetical prote
26	43	37.7	490	2 AC2458	hypothetical prote
27	43	37.7	2907	2 A57278	fibrillin-2 precur
28	43	37.7	2918	2 A54105	fibrillin-2 precur
29	42	36.8	99	2 H72868	AcOrf-150 protein

30	42	36.8	174	2 H96001	hypothetical prote
31	42	36.8	232	2 S56275	probable membrane
32	42	36.8	440	2 T24323	hypothetical prote
33	42	36.8	516	2 AH2417	hypothetical prote
34	42	36.8	1462	1 B36182	protein-tyrosine-p
35	42	36.8	4543	1 A53102	alpha-2-macroglobu
36	41.5	36.4	1847	2 T18308	probable vitelloge
37	41.5	36.4	1984	2 T13171	probable vitelloge
38	41	36.0	108	2 B87095	ferredoxin (impor
39	41	36.0	108	2 A70876	probable ferredoxi
40	41	36.0	115	2 T41887	AcMNPV orf150 - Bo
41	41	36.0	283	2 S75226	esterase elr1916 -
42	41	36.0	291	2 H97090	thioredoxin reduct
43	41	36.0	366	2 D45558	epidermal growth f
44	41	36.0	387	2 JE0360	gamma-Butyrobetain
45	41	36.0	414	2 PS0323	von Willebrand fac
46	41	36.0	424	2 B38176	samb protein - Sal
47	41	36.0	506	2 S71591	aspartic proteinas
48	41	36.0	1401	2 S77657	cyclic peptide syn
49	41	36.0	1717	1 A45558	epidermal growth f
50	41	36.0	2150	2 T32497	hypothetical prote
51	40.5	35.5	341	2 T19924	hypothetical prote
52	40.5	35.5	770	2 T00203	LDL receptor-relat
53	40.5	35.5	1297	2 T30274	protocollaisin - se
54	40.5	35.5	3871	2 T22812	hypothetical prote
55	40	35.1	105	2 S08287	ferredoxin (4Fe-4S
56	40	35.1	106	1 FEMVFS	ferredoxin (3Fe-4S
57	40	35.1	121	2 G64152	hypothetical prote
58	40	35.1	136	2 A85711	probable IS encode
59	40	35.1	195	2 AC0123	probable exported
60	40	35.1	206	2 D91109	hypothetical prote
61	40	35.1	261	2 D83101	conserved hypotet
62	40	35.1	261	2 G85954	unknown protein en
63	40	35.1	297	2 S04455	hypothetical prote
64	40	35.1	303	1 GEHUN	osteonectin precur
65	40	35.1	304	1 GEBON	osteonectin precur
66	40	35.1	304	2 S04456	hypothetical prote
67	40	35.1	330	2 S60211	fomB protein - Str
68	40	35.1	348	2 T29288	hypothetical prote
69	40	35.1	354	2 T22274	hypothetical prote
70	40	35.1	392	2 H97026	flavoprotein limpo
71	40	35.1	427	2 G00039	von Willebrand fac
72	40	35.1	434	2 T21995	hypothetical prote
73	40	35.1	463	2 B91112	hypothetical prote
74	40	35.1	468	2 H72230	glutamate synthase
75	40	35.1	468	2 T50873	hypothetical prote
76	40	35.1	512	2 B90670	hypothetical prote
77	40	35.1	512	2 H90766	hypothetical prote
78	40	35.1	512	2 C90792	hypothetical prote
79	40	35.1	512	2 D90836	hypothetical prote
80	40	35.1	512	2 B90856	hypothetical prote
81	40	35.1	512	2 H90906	hypothetical prote
82	40	35.1	512	2 G90977	hypothetical prote
83	40	35.1	512	2 C91197	hypothetical prote
84	40	35.1	512	2 A85653	unknown protein en
85	40	35.1	512	2 A86044	hypothetical prote
86	40	35.1	614	2 T19963	hypothetical prote
87	40	35.1	667	2 S48285	probable glycine-t
88	40	35.1	1064	2 T50127	hypothetical prote
89	40	35.1	1260	2 H64516	hypothetical prote
90	40	35.1	1260	2 S60896	agglutinin-like pr
91	40	35.1	1437	2 F96783	unknown protein P2
92	40	35.1	2233	2 T28669	surface protein 51
93	39.5	34.6	129	2 A72606	hypothetical prote
94	39.5	34.6	251	2 F98785	formate acetyltran
95	39.5	34.6	357	2 S38338	naringenin 3-dioxy
96	39.5	34.6	358	2 T45755	flavanone 3-hydrox
97	39.5	34.6	1172	1 TSHUP2	thrombospondin 2 p
98	39.5	34.6	1172	2 A42587	thrombospondin 2 p
99	39.5	34.6	2180	2 T29764	hypothetical prote
100	39	34.2	114	2 E70759	probable foxA prot

ALIGNMENTS

```
RESULT 1
A24571
protein-tyrosine kinase (EC 2.7.1.112) erbB2 precursor - human
N:Alternate names: c-erb-B-2 protein precursor; Kinase-related transforming protein erbB
C:Species: Homo sapiens (man)
C>Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 05-Oct-2004
C:Accession: A24571; A25491; A44188; B44188; I59509; I57622
R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f
A:Reference number: A24571; MUID:86118663; PMID:3003577
A:Accession: A24571
A:Molecule type: mRNA
A:Residues: 1-1255 <YAM>
A:Cross-references: UNIPROT:P04626; UNIPARC:UPI000003F55F; GB:X03363; NID:g31197; PIDN:C
R:Semba, K.; Kanata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm
A:Reference number: A25491; MUID:86016729; PMID:2995967
A:Accession: A25491
A:Molecule type: DNA
A:Residues: 737-1031 <SEM>
A:Cross-references: UNIPARC:UPI000016A8A7; GB:M11767; NID:g182163; PIDN:AAA35808.1; PID:
R:Cousens, L.; Yang-Feng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, P
Science 230, 1132-1139, 1985
A:Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromo
A:Reference number: A44188; MUID:86070181; PMID:2999974
A:Accession: A44188
A:Molecule type: DNA
A:Residues: 740-910 <COU1>
A:Cross-references: UNIPARC:UPI000016AA26; GB:M12036; NID:g183988; PIDN:AAA35978.1; PID:
A:Accession: B44188
A:Molecule type: mRNA
A:Residues: 1-517, 'RALH', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <COU2>
A:Cross-references: UNIPARC:UPI00001725C7; GB:M11730; NID:g183986
R:King, C.R.; Kraus, M.H.; Aaronson, S.A.
Science 229, 974-976, 1985
A:Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
A:Reference number: I59509; MUID:85272597; PMID:2992089
A:Accession: I59509
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 832-909 <REX>
A:Cross-references: UNIPARC:UPI0000070A3F; GB:L29395; NID:g459807; PIDN:AAA35809.1; PID:
R:Pal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
Mol. Cell. Biol. 7, 2597-2601, 1987
A:Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
A:Reference number: I57622; MUID:87286898; PMID:3039351
A:Accession: I57622
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-191 <TAL>
A:Cross-references: UNIPARC:UPI0000000427; GB:M16792; NID:g183983; PIDN:AAA58637.1; PID:
C:Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
C:Genetics:
A:Gene: GDB:ERBB2; NGL; NEU; HER-2
A:Cross-references: GDB:120613; OMIM:164870
A:Map position: 17q21.1-17q21.1
A:Introns: 25/1; 75/3; 147/1; 883/3
A>Note: the list of introns is incomplete
C:Function:
A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C:Keywords: ATP; autophosphorylation; duplication; Glycoprotein; phosphoprotein; phospho
inase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <WAT>
F:22-653/Domain: extracellular #status predicted <EXT>
F:70-304/Domain: EGF receptor extracellular domain repeat <EE1>
F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>
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F:654-675/Domain: transmembrane #status predicted <TMM>
F:676-1255/Domain: intracellular #status predicted <INT>
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif
F:68124,187,259,530,571,629/Binding site: carbohydate (Asn) (covalent) #status predict
F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
F:753/Active site: Lys #status predicted
F:1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)

Query Match 92.1%; Score 105; DB 1; Length 1255;
Best Local Similarity 95.0%; Pred. No. 5.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTSCVDLDDKGCPEAQR 20
||| ||||| ||||| ||||| |||||
Db 628 INCTHSCVDLDDKGCPEAQR 647

RESULT 2
I48161
p-185 precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C:Accession: I48161
R:Nakamura, T.; Ushijima, T.; Ishizaka, T.; Nagao, M.; Arai, M.; Yamazaki, Y.; Ishikawa,
Gene 140, 251-255, 1994
A:Title: Cloning and activation of the Syrian hamster neu proto-oncogene.
A:Reference number: I48161; MUID:94193007; PMID:7908275
A:Accession: I48161
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1254 <RES>
A:Cross-references: UNIPROT:Q60553; UNIPARC:UPI000012A111; GB:D16295; NID:g4932336; PIDN:
C:Genetics:
A:Gene: neu
C:Superfamily: Tyrosine-protein kinase, EGF receptor type; protein kinase homology
C:Keywords: ATP
F:718-983/Domain: protein kinase homology <KIN>
F:726-734/Region: protein kinase ATP-binding motif

Query Match 86.0%; Score 98; DB 2; Length 1254;
Best Local Similarity 85.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 INGTSCVDLDDKGCPEAQR 20
||| ||||| ||||| ||||| |||||
Db 628 INCTHSCVDLDDKGCPEAQR 647

RESULT 3
TVRTNU
protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
C:Accession: A24562; A61204
R:Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
Nature 319, 226-230, 1986
A:Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
A:Reference number: A24562; MUID:86118662; PMID:3945311
A:Accession: A24562
A:Molecule type: mRNA
A:Residues: 1-1260 <BAR>
R:Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen,
Carcinogenesis 12, 1975-1978, 1991
A:Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no
2-thiazolylformamide or N-methyl-N-nitrosourea.
A:Reference number: A61204; MUID:92035293; PMID:1682063
A:Accession: A61204
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 637-663, 'V', 665-702 <MAS>
A:Cross-references: UNIPARC:UPI00001725C8
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OM protein - protein search, using sw model

Run on: December 3, 2005, 07:35:08 ; Search time 132.727 Seconds
(without alignments)
106.312 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVDLDDRCPPAEQR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	105	92.1	435	2 Q6ZMM4_HUMAN	P04626 homo sapien
2	105	92.1	1255	1 ERBB2_HUMAN	Q923V5 rattus norv
3	98	86.0	176	2 Q923V5_RAT	Q80Y89 mus musculu
4	98	86.0	711	2 Q80Y89_MOUSE	Q80C07 m mus muscu
5	98	86.0	881	2 Q80C07_MOUSE	P06494 rattus norv
6	98	86.0	1254	1 ERBB2_MESAU	P06494 rattus norv
7	98	86.0	1257	1 ERBB2_RAT	Q8K3F9 rattus norv
8	98	86.0	1259	2 Q8K3F9_RAT	Q6ZPE0 mus musculu
9	98	86.0	1305	2 Q6ZPE0_MOUSE	O18735 canis fami
10	97	85.1	1259	1 ERBB2_CANFA	Q411T0 gibberella
11	61	53.5	311	2 Q411T0_GIBZE	O5EBY4 brachydanio
12	54.5	47.8	1275	2 Q5EBY4_BRARE	Q7YQX5 phascogale
13	53	46.5	293	2 Q7YQX5_PHATA	Q7YQX4 sminthopsis
14	53	46.5	305	2 Q7YQX4_9META	Q7YQX3 dasyurus al
15	53	46.5	314	2 Q7YQX3_DASAL	Q7YQY0 dromiclops
16	53	46.5	322	2 Q7YQY0_DRONU	P41798 kluyveromyc
17	51	44.7	235	1 RS6_KLUMA	Q9FEI1 avena pilos
18	51	44.7	287	2 Q9FEI1_9POAL	Q9FEJ2 avena claud
19	51	44.7	287	2 Q9FEJ2_9POAL	Q9FEJ3 avena ventr
20	51	44.7	287	2 Q9FEJ3_9POAL	Q4RG29 tetraodon n
21	51	44.7	1335	2 Q4RG29_TETNG	Q9PJM4 chlamydia m
22	50	43.9	122	1 RL14_CHLMU	Q9PJM4 chlamydia p
23	50	43.9	122	1 RL14_CHLPN	P28533 chlamydia t
24	50	43.9	122	1 RL14_CHLTR	Q6CM04 kluyveromyc
25	50	43.9	236	1 RS6_KLULA	Q754G9 ashbya gose
26	50	43.9	972	2 Q754G9_ASHGO	Q9PTY3 paralichthy
27	49.5	43.4	805	2 Q9PTY3_PAROL	Q86DY7 schistosoma
28	49	43.0	243	2 Q86DY7_SCHJA	Q9HNV3 halobacteri
29	49	43.0	303	2 Q9HNV3_HALSA	Q29134 tupaiia glis
30	49	43.0	358	2 Q29134_TUPGL	Q9TV39 tupaiia glis
31	49	43.0	358	2 Q9TV39_TUPGL	

32	49	43.0	409	2 Q28549_ORYAF	Q28549 orycteropis
33	49	43.0	766	2 Q4P734_USTMA	Q4P734 ustilago ma
34	48	42.1	140	2 Q4TCV6_TETNG	Q4TCV6 tetraodon n
35	48	42.1	145	2 Q9F560_ECOLI	Q9F560 escherichia
36	48	42.1	287	2 Q9FEI5_9POAL	Q9FEI5 avena macro
37	48	42.1	323	2 Q7YQX9_NORTY	Q7YQX9 notoryctes
38	48	42.1	372	2 Q28449_LOXAF	Q28449 loxodonta a
39	48	42.1	388	2 Q4RIL8_TETNG	Q4RIL8 tetraodon a
40	48	42.1	411	2 Q28404_ELEMA	Q28404 elephas max
41	48	42.1	411	2 Q8WMS8_TRIMA	Q8WMS8 trichechus
42	48	42.1	425	2 Q28759_PROCA	Q28759 procavia ca
43	48	42.1	427	2 Q28352_DUGDU	Q28352 dugong dugo
44	47	41.2	220	2 Q59ZS3_CANAL	Q59ZS3 candida alb
45	47	41.2	299	2 Q6QXH9_GVAS	Q6QXH9 agrotis seg
46	47	41.2	319	2 Q8HXM6_9EUTH	Q8HXM6 uropailus s
47	47	41.2	344	2 Q7YQY1_PHACI	Q7YQY1 phascolarct
48	47	41.2	344	2 Q86621_VOMOR	Q86621 vomphatus ur
49	47	41.2	353	2 Q9SP47_EPIPO	Q9SP47 epiphyas po
50	47	41.2	402	2 Q5XI84_RAT	Q5XI84 rattus norv
51	47	41.2	443	1 FBLN4_CRIGR	Q55058 cricetus
52	47	41.2	443	1 FBLN4_HUMAN	Q95957 homo sapien
53	47	41.2	443	1 FBLN4_MOUSE	Q9WVJ9 mus musculu
54	47	41.2	443	2 Q6FH22_HUMAN	Q6FH22 homo sapien
55	47	41.2	443	2 Q96TF5_HUMAN	Q96TF5 homo sapien
56	47	41.2	443	2 Q9H3D5_HUMAN	Q9H3D5 homo sapien
57	47	41.2	443	2 Q542X5_MOUSE	Q542X5 mus musculu
58	47	41.2	443	2 Q9JM06_MOUSE	Q9JM06 mus musculu
59	47	41.2	534	2 Q57TS0_9TRYP	Q57TS0 trypanosoma
60	47	41.2	542	2 Q8S7G1_ORYSA	Q8S7G1 oryza sativ
61	47	41.2	620	2 Q59G18_HUMAN	Q59G18 homo sapien
62	47	41.2	1435	1 DP03_MYCPU	P47729 mycoplasma
63	47	41.2	2691	2 Q4QFA9_LEIMA	Q4QFA9 leishmania
64	46.5	40.8	146	2 Q42178_ARATH	Q42178 arabidopsis
65	46.5	40.8	161	2 Q96FH9_HUMAN	Q96FH9 homo sapien
66	46.5	40.8	260	2 Q5VXB4_HUMAN	Q5VXB4 homo sapien
67	46.5	40.8	349	2 Q9NVG4_HUMAN	Q9NVG4 homo sapien
68	46.5	40.8	365	2 Q4URH9_XANCP	Q4URH9 xanthomonas
69	46.5	40.8	365	2 Q8PC19_XANCP	Q8PC19 xanthomonas
70	46.5	40.8	370	2 Q6FWK6_CANGA	Q6FWK6 candida gla
71	46.5	40.8	494	2 Q8IWV5_HUMAN	Q8IWV5 homo sapien
72	46.5	40.8	548	2 Q21629_CABEL	Q21629 caenorhabdi
73	46.5	40.8	549	2 Q9HOD0_HUMAN	Q9HOD0 homo sapien
74	46.5	40.8	572	2 Q9HC49_HUMAN	Q9HC49 homo sapien
75	46.5	40.8	682	2 Q8IWV6_HUMAN	Q8IWV6 homo sapien
76	46.5	40.8	682	2 Q9H988_HUMAN	Q9H988 homo sapien
77	46.5	40.8	683	2 Q9H012_HUMAN	Q9H012 homo sapien
78	46.5	40.8	683	2 Q8WVK9_HUMAN	Q8WVK9 homo sapien
79	46	40.4	122	2 Q5L710_CHLAB	Q5L710 chlamydophi
80	46	40.4	122	2 Q824P1_CHLCV	Q824P1 chlamydophi
81	46	40.4	236	1 RS6_DBBHA	Q6BKH8 debaryomyce
82	46	40.4	284	2 Q61G31_CAEBR	Q61G31 caenorhabdi
83	46	40.4	327	1 EXOB_RHILT	Q59745 rhizobium l
84	46	40.4	385	2 Q91YC1_9RODE	Q91YC1 phodopus ro
85	46	40.4	385	2 Q91YC6_9RODE	Q91YC6 myospalax s
86	46	40.4	385	2 Q91YF8_MESAU	Q91YF8 mesocricetu
87	46	40.4	385	2 Q91YH1_CRIMI	Q91YH1 cricetus
88	46	40.4	410	2 Q841K7_9ACTO	Q841K7 streptomyc
89	46	40.4	462	1 ILERA_RAT	P22273 rattus norv
90	46	40.4	711	2 Q4M193_9BURK	Q4M193 burkholderi
91	46	40.4	2924	2 Q722C2_TOXGO	Q722C2 toxoplasma
92	45.5	39.9	567	2 Q63MT4_BURPS	Q63MT4 burkholderi
93	45.5	39.9	567	2 Q62DG8_BURMA	Q62DG8 burkholderi
94	45.5	39.9	1111	2 Q80YNA_RAT	Q80YNA rattus norv
95	45.5	39.9	1242	2 Q57U99_9TRYP	Q57U99 trypanosoma
96	45	39.5	111	2 Q9X898_STRCO	Q9X898 streptomyc
97	45	39.5	140	2 Q6G6J6_STAAS	Q6G6J6 staphylococ
98	45	39.5	140	2 Q6GDM1_STAAR	Q6GDM1 staphylococ
99	45	39.5	140	2 Q5HD77_STAAC	Q5HD77 staphylococ
100	45	39.5	140	2 Q7A3M1_STAAN	Q7A3M1 staphylococ

ALIGNMENTS

```

RESULT 1
Q62MM4 HUMAN
ID Q62MM4_HUMAN PRELIMINARY; PRT; 435 AA.
AC Q62MM4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein FLJ16821.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=86118663; PubMed=3003577;
RA Yamamoto T., Ikawa S., Akiyama T., Senba K., Nomura N., Miyajima N.,
Saito T., Toyoshima K.;
"Similarity of protein encoded by the human c-erb-B-2 gene to
epidermal growth factor receptor.";
RL Nature 319:230-234(1986).
[2]
RN NUCLEOTIDE SEQUENCE, AND VARIANT ALA-1170.
RX MEDLINE=86070181; PubMed=2999974;
RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A., McGrath J.,
Seeburg P.H., Libermann T.A., Schlessinger J., Francke U.,
Levinson A., Ullrich A.;
"Tyrosine kinase receptor with extensive homology to EGF receptor
shares chromosomal location with neu oncogene.";
RL Science 230:1132-1139(1985).
[3]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS CYS-452; VAL-655 AND
ALA-1170.
RX Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
"NIHES-SNPs, environmental genome project, NIHES ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[4]
RN NUCLEOTIDE SEQUENCE OF 1-191.
RX MEDLINE=87286898; PubMed=3039351;
RA Tal M., King C.R., Kraus M.H., Ullrich A., Schlessinger J., Givol D.;
"Human HER2 (neu) promoter: evidence for multiple mechanisms for
transcriptional initiation.";
RL Mol. Cell. Biol. 7:2597-2601(1987).
[5]
RN NUCLEOTIDE SEQUENCE OF 737-1031.
RX MEDLINE=86016729; PubMed=2995967;
RA Semba K., Kamata N., Toyoshima K., Yamamoto T.;
"A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-
erbB-1/epidermal growth factor-receptor gene and is amplified in a
human salivary gland adenocarcinoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).
[6]
RN NUCLEOTIDE SEQUENCE OF 832-909.
RX TISSUE=Mammary carcinoma;
RA King C.R., Kraus M.H., Aaronson S.A.;
"Amplification of a novel v-erbB-related gene in a human mammary
carcinoma.";
RL Science 229:974-976(1985).
[7]
RN NUCLEOTIDE SEQUENCE OF 1081-1245, AND VARIANT ALA-1170.
RX MEDLINE=94000386; PubMed=8104414;
RA Sarkar F.H., Ball D.E., Li Y.W., Crissman J.D.;
"Molecular cloning and sequencing of an intron of Her-2/neu (ERBB2)
gene.";
RL DNA Cell Biol. 12:611-615(1993).
[8]
RN IDENTIFICATION IN A COMPLEX WITH PIK3C2A AND EGFR, IDENTIFICATION IN A
COMPLEX WITH PIK3C2B AND EGFR, AND INTERACTION WITH PIK3C2B.
RX PubMed=10805725;
RA Arcaro A., Zvelebil M.J., Wallasch C., Ullrich A., Waterfield M.D.,
Domin J.;
"Class II phosphoinositide 3-kinases are downstream targets of
activated polypeptide growth factor receptors.";
RL Mol. Cell. Biol. 20:3817-3830(2000).
[9]
RN INTERACTION WITH PLXNB1.
RX PubMed=15210733; DOI=10.11083/jcb.200312094;
RA Swiercz J.M., Kuner R., Offermanns S.;

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Query Match 92.1%; Score 105; DB 2; Length 435;
Best Local Similarity 95.0%; Pred. No. 5.7e-08;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 INGTSCVDLDDKGCFAEQR 20
DQ 178 INCTHSCVDLDDKGCFAEQR 197

```

```

RESULT 2
ERBB2 HUMAN
ID ERBB2_HUMAN STANDARD; PRT; 1255 AA.
AC P04626; Q14256; Q6LDV1; Q9UMK4;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Receptor tyrosine-protein kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (C-erbB-2) (NEU proto-oncogene) (Tyrosine kinase-type cell
surface receptor HER2) (MLN 19).
GN Name=ERBB2; Synonyms=HER2, NEU, NGL;
OS Homo sapiens (Human).

```

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 22:22:28 ; Search time 1834.09 Seconds
(without alignments)
619.854 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVDLDDKGPAAQR 20

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09632036/runat_02122005_104140_25811/app_query.fasta_1.398
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09632036 @CGN 1 1 3563 @runat_02122005_104140_25811 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_ov:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_ets:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	105	92.1	201	6	AR229723 Sequence
2	105	92.1	499	6	CS085267 Sequence
3	105	92.1	739	6	CS085266 Sequence

4	105	92.1	922	6	CS085259 Sequence
5	105	92.1	979	6	CS085265 Sequence
6	105	92.1	1219	6	CS085264 Sequence
7	105	92.1	1459	6	CS085263 Sequence
8	105	92.1	1699	6	CS085262 Sequence
9	105	92.1	1939	6	CS085261 Sequence
10	105	92.1	2028	6	CS020247 Sequence
11	105	92.1	2028	6	CS020248 Sequence
12	105	92.1	2083	6	CS085260 Sequence
13	105	92.1	2086	6	CS085268 Sequence
14	105	92.1	2086	6	CS085269 Sequence
15	105	92.1	2086	6	CS085270 Sequence
16	105	92.1	2086	6	CS085271 Sequence
17	105	92.1	2086	6	CS085272 Sequence
18	105	92.1	2320	6	CS075235 Sequence
19	105	92.1	2385	6	AR082744 Sequence
20	105	92.1	2385	6	AR099963 Sequence
21	105	92.1	2385	6	AR143949 Sequence
22	105	92.1	2437	6	CS075247 Sequence
23	105	92.1	2871	6	BD222937 Heteromin
24	105	92.1	2871	6	AX023363 Sequence
25	105	92.1	3678	6	AX050514 Sequence
26	105	92.1	3768	6	AR034479 Sequence
27	105	92.1	3768	6	BD224136 Sequence
28	105	92.1	3768	6	BD267514 Sequence
29	105	92.1	3768	6	CO815384 Sequence
30	105	92.1	3768	6	CO841302 Sequence
31	105	92.1	3768	6	CO841343 Sequence
32	105	92.1	3768	6	CO841344 Sequence
33	105	92.1	3768	6	CS007994 Sequence
34	105	92.1	3768	6	CS020239 Sequence
35	105	92.1	3768	6	CS104222 Sequence
36	105	92.1	3768	6	AR409603 Sequence
37	105	92.1	3768	6	AX060704 Sequence
38	105	92.1	3768	6	AX201817 Sequence
39	105	92.1	3768	6	AX380923 Sequence
40	105	92.1	3768	6	AX384604 Sequence
41	105	92.1	3768	6	AX465456 Sequence
42	105	92.1	3768	6	AX467229 Sequence
43	105	92.1	3768	6	AX481438 Sequence
44	105	92.1	3768	11	AY888050 Synthetic
45	105	92.1	3768	11	AY888051 Synthetic
46	105	92.1	3768	11	AY888102 Synthetic
47	105	92.1	3768	11	AY888103 Synthetic
48	105	92.1	3768	11	AY888104 Synthetic
49	105	92.1	3778	6	CS020249 Sequence
50	105	92.1	4473	6	AR080259 Sequence
51	105	92.1	4473	6	AR167390 Sequence
52	105	92.1	4473	6	AR392088 Sequence
53	105	92.1	4473	6	AR534814 Sequence
54	105	92.1	4473	8	HSERB2R
55	105	92.1	4483	6	CQ723568 Sequence
56	105	92.1	4530	6	CO834023 Sequence
57	105	92.1	4530	6	CQ873909 Sequence
58	105	92.1	4530	6	CQ977093 Sequence
59	105	92.1	4530	6	CS052366 Sequence
60	105	92.1	4530	6	CS063102 Sequence
61	105	92.1	4530	6	CS080883 Sequence
62	105	92.1	4530	6	CS101342 Sequence
63	105	92.1	4530	6	CS103534 Sequence
64	105	92.1	4530	6	I21124 Sequence 9
65	105	92.1	4530	6	I59745 Sequence 9
66	105	92.1	4530	6	AR202597 Sequence
67	105	92.1	4530	6	AR283481 Sequence
68	105	92.1	4530	6	AR344811 Sequence
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71	105	92.1	4530	6	AX644071 Sequence
72	105	92.1	4530	6	AX771418 Sequence
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76	105	92.1	4536	8	BC080193 Homo sapi

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77 105 92.1 4647 6 CS075243 Sequence
78 105 92.1 4932 6 CQ853478 Sequence
79 105 92.1 4932 8 AK131568 Homo sapi
80 105 92.1 5661 6 CQ975755 Sequence
81 105 92.1 9274 6 AR409602 Sequence
82 105 92.1 9274 6 AX060703 Sequence
83 100 87.7 3768 6 CQ841341 Sequence
84 98 86.0 528 9 AF393158 Rattus no
85 98 86.0 2763 6 AX380942 Sequence
86 98 86.0 2781 6 AX380944 Sequence
87 98 86.0 3771 6 BD267516 HER-2/neu
88 98 86.0 3771 6 AX189662 Sequence
89 98 86.0 3771 6 AX380925 Sequence
90 98 86.0 3955 6 BD267515 Sequence
91 98 86.0 3955 6 I21129 Sequence 14
92 98 86.0 3955 6 I59750 Sequence 14
93 98 86.0 3955 6 AX380924 Sequence
94 98 86.0 3955 9 RNNEUR
95 98 86.0 4062 9 HAMNEU
96 98 86.0 4478 9 BC061863
97 98 86.0 4506 9 AK129487 Rattus no
98 86.0 4694 9 BC046811 Mus muscu
99 98 86.0 4695 9 BC053078 Mus muscu
100 98 86.0 4727 9 AY116182 Rattus no
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ALIGNMENTS

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AR229723 LOCUS AR229723 201 bp RNA linear PAT 20-DEC-2002
DEFINITION Sequence 3 from patent US 6451524.
ACCESSION AR229723
VERSION AR229723.1 GI:27269547
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 201)
AUTHORS Ecker,D.J.
TITLE Identification of disease predictive nucleic acids
JOURNAL Patent: US 6451524-A 3 17-SEP-2002;
ISIS Pharmaceuticals, Inc.; Carlsbad, CA
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Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 6 Gaps: 0
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US-09-632-036F-42 (1-20) x AR229723 (1-201)

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RESULT 2
CS085267 LOCUS CS085267 499 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 9 from Patent WO2005039618.
ACCESSION CS085267
VERSION CS085267.1 GI:66711224
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
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REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu /sp -encoding DNA and Therapeutical uses thereof
JOURNAL Patent: WO 2005039618-A 9 06-MAY-2005;
Indena S.p.A. (IT)
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Score: 105.00 Matches: 19
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Query Match: 92.11% Indels: 0
DB: 6 Gaps: 0
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US-09-632-036F-42 (1-20) x CS085267 (1-499)

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CS085266 LOCUS CS085266 739 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 8 from Patent WO2005039618.
ACCESSION CS085266
VERSION CS085266.1 GI:66711223
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
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REFERENCE 1
AUTHORS Amici,A., Cavallo,F., Forni,G. and Marchini,C.
TITLE P185 sp neu /sp -encoding DNA and Therapeutical uses thereof
JOURNAL Patent: WO 2005039618-A 8 06-MAY-2005;
Indena S.p.A. (IT)
FEATURES
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/db_xref="taxon:32644"
ORIGIN
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Alignment Scores:

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Percent Similarity: 95.00% Conservative: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 6 Gaps: 0
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US-09-632-036F-42 (1-20) x CS085266 (1-739)

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RESULT 4
CS085259 LOCUS CS085259 922 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 1 from Patent WO2005039618.
ACCESSION CS085259
VERSION CS085259.1 GI:66711216
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 21:10:38 ; Search time 235.909 Seconds
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565.022 Million cell updates/sec

Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVDLDDKCPAEQR 20

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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-DB=N_Geneseq -QFMT=fastcap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=100
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09632036 @CGN 1.1 714 @runat_02122005_104140_25801 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	105	92.1	201	3	AAA62125	Aaa62125 Her2 norm
2	105	92.1	499	14	ADZ69878	Adz69878 p185neu o
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4	105	92.1	739	14	ADZ69877	Adz69877 p185neu o

5	105	92.1	884	10	ADG17941	AdG17941 Human HER
6	105	92.1	922	14	ADZ69870	Adz69870 p185neu o
7	105	92.1	979	14	ADZ69876	Adz69876 p185neu o
8	105	92.1	1219	14	ADZ69875	Adz69875 p185neu o
9	105	92.1	1459	14	ADZ69874	Adz69874 p185neu o
10	105	92.1	1479	10	ADG17935	AdG17935 Human HER
11	105	92.1	1699	14	ADZ69873	Adz69873 p185neu o
12	105	92.1	1939	14	ADZ69872	Adz69872 p185neu o
13	105	92.1	1956	12	ADJ57171	AdJ57171 Her-2/neu
14	105	92.1	2028	14	ADM87396	AdM87396 Human cod
15	105	92.1	2028	14	ADM87397	AdM87397 Human wil
16	105	92.1	2052	12	ADJ57170	AdJ57170 Human Her
17	105	92.1	2083	14	ADZ69871	Adz69871 p185neu o
18	105	92.1	2086	14	ADZ69880	Adz69880 p185neu o
19	105	92.1	2086	14	ADZ69879	Adz69879 p185neu o
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22	105	92.1	2086	14	ADZ69883	Adz69883 p185neu o
23	105	92.1	2125	2	AAV21727	AAV21727 Humanised
24	105	92.1	2149	10	ADG17943	AdG17943 Human HER
25	105	92.1	2164	10	ADM17939	AdM17939 Human HER
26	105	92.1	2261	11	ADM29355	AdM29355 Human nov
27	105	92.1	2320	14	ADZ47794	AdZ47794 DNA encod
28	105	92.1	2385	2	AAT72725	AAT72725 Her2-GM-C
29	105	92.1	2437	14	ADZ47806	AdZ47806 DNA encod
30	105	92.1	2802	13	ADT50728	AdT50728 Cancer re
31	105	92.1	2871	3	AZ50586	Az50586 DC8cFV-e
32	105	92.1	3188	11	ADM29351	AdM29351 Human nov
33	105	92.1	3600	3	AAA89736	AAA89736 Human HER
34	105	92.1	3678	6	ABK86207	ABk86207 cDNA enc
35	105	92.1	3765	10	ADB67620	ADb67620 Human epi
36	105	92.1	3765	14	ADZ72379	AdZ72379 DNA encod
37	105	92.1	3768	2	AAT40739	AAT40739 HER-2/neu
38	105	92.1	3768	2	AAx01912	Aax01912 Human HER
39	105	92.1	3768	3	AAA09455	AAA09455 Human her
40	105	92.1	3768	5	AAH23392	Aah23392 Human HER
41	105	92.1	3768	6	ABV78168	ABv78168 Human ERB
42	105	92.1	3768	6	ABZ35744	ABz35744 Human ERB
43	105	92.1	3768	6	AAD32743	AAd32743 Human HER
44	105	92.1	3768	6	ABK10730	ABk10730 Human HER
45	105	92.1	3768	6	AAH43935	AAh43935 Human HER
46	105	92.1	3768	6	ABX09987	ABx09987 Human ERB
47	105	92.1	3768	6	AAH43986	AAh43986 Human HER
48	105	92.1	3768	6	ABK14058	ABk14058 Human HER
49	105	92.1	3768	6	ABA92250	ABa92250 Human Her
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51	105	92.1	3768	8	ACC57649	Acc57649 Human pro
52	105	92.1	3768	13	ADQ75970	AdQ75970 Rhesus mo
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69	105	92.1	4478	12	ADQ83974	AdQ83974 Human tum
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72	105	92.1	4530	2	AAT71253	Aat71253 Human HER
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ALIGNMENTS

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ID AAA62125 standard; RNA; 201 BP.
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AC AAA62125;
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DT 20-JUN-2001 (first entry)
XX
DE Her2 normal form transcript.
XX
KW Her2; disease prediction; breast cancer; human; tyrosine kinase; ss.
XX
OS Homo sapiens.
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FH Key Location/Qualifiers
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PN WO200031110-A1.
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PD 02-JUN-2000.
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XX 22-NOV-1999; 99WO-US027710.
XX
PR 25-NOV-1998; 98US-00200355.
XX 25-NOV-1999; 98US-0110024P.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Ecker DJ;
XX
XX WPI; 2000-400027/34.
XX
PT Identifying a target nucleic acid sequence predictive of preselected
PT disease states such as a cancerous state, by comparing members of a set
PT of mRNA molecules, from a common gene, containing different sequences and
PT structures.
XX
PS Example 2; Fig 3; 38pp; English.
XX
CC The HER2 proto-oncogene encodes a tyrosine kinase receptor, which
CC functions in cellular signal transduction. The HER2 protein is implicated
CC in breast cancer. The HER2 receptor mRNA exists in at least two forms: a
CC normal form and a truncated form. The present sequence is the normal form
CC RNA of HER2. The truncated form RNA sequence of HER2 (AAA62126) encodes a
CC protein associated with increased resistance to the growth inhibiting
CC effects of a monoclonal antibody, Herceptin, used in cancer treatment.
CC The truncated form of the transcript contains unique structures not found
CC in the normal form. The present sequence is predictive of Herceptin-
CC resistant cancer and detection of the present sequence may therefore be
CC used as a method of diagnosing breast cancer. Other diseases which may be
CC identified by using a similar method to detect other RNA molecules are
CC hyperproliferative conditions, Lupus erythematosus, psoriasis,
CC inflammation, cardiovascular disease, pain, arthritis, obesity, trauma,
CC Huntington's disease or neurological disorders
XX
SQ Sequence 201 BP; 34 A; 67 C; 56 G; 0 T; 44 U; 0 Other;

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Alignment Scores:
Pred. No.: 6.36e-08 Length: 201
Score: 105.00 Matches: 19
Percent Similarity: 95.00% Conservatives: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 3 Gaps: 0
US-09-632-036F-42 (1-20) x AAA62125 (1-201)

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QY 1 IleAenGlyThrHisSerCysValAspLeuAspLysGlyCysProAlaGluInArg 20

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 10, 2005, 22:40:44 ; Search time 78.1818 Seconds
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454.725 Million cell updates/sec

Title: US-09-632-036F-42
Perfect score: 114
Sequence: 1 INGTSCVDLDDKCPAEQR 20

Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Database : Issued Patents NA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	105	92.1	2385	2	US-09-146-283-3
3	105	92.1	2385	3	US-08-579-823A-3
4	105	92.1	2385	3	US-09-344-195-3
5	105	92.1	3768	2	US-08-625-101-1
6	105	92.1	3768	2	US-08-356-786-1
7	105	92.1	3768	3	US-09-811-115-2
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12	105	92.1	4473	3	US-09-441-411-5
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15	105	92.1	4530	3	US-09-167-322-4
16	105	92.1	4530	3	US-09-527-487-1
17	105	92.1	4530	3	US-09-877-177A-11
18	105	92.1	9274	3	US-09-811-115-1
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21	85	74.6	1872	3	US-08-422-108-2
22	85	74.6	1872	3	US-08-422-73A-2
23	68	59.6	153	3	US-08-776-251-3
24	68	59.6	816	3	US-08-776-251-10
25	51.5	45.2	601	3	US-09-949-016-26918
26	51.5	45.2	601	3	US-09-949-016-26919
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35	50	43.9	123030	3	US-09-438-185A-1
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38	48	42.1	306	2	US-08-313-185-63
39	48	42.1	306	3	US-09-082-614A-63
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83 45.5 39.9 3083 3 US-09-694-777A-2 Sequence 2, Appli
84 45 39.5 374 3 US-09-270-767-40 Sequence 40, Appl
85 45 39.5 374 3 US-09-270-767-15322 Sequence 15322, A
86 45 39.5 519 3 US-09-621-976-10460 Sequence 10460, A
87 45 39.5 531 4 US-09-605-703B-2597 Sequence 2597, Ap
88 45 39.5 612 3 US-09-248-796A-1530 Sequence 1530, Ap
89 45 39.5 700 3 US-09-735-271-61 Sequence 61, Appl
90 45 39.5 737 3 US-09-533-559-4539 Sequence 4539, Ap
91 45 39.5 1029 3 US-09-902-540-8675 Sequence 8675, Ap
92 45 39.5 1108 2 US-07-866-560-5 Sequence 5, Appli
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94 45 39.5 1108 2 US-08-478-992-5 Sequence 5, Appli
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98 45 39.5 1108 3 US-09-542-122-5 Sequence 5, Appli
99 45 39.5 1108 3 US-09-353-099-9 Sequence 9, Appli
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ALIGNMENTS

RESULT 1
US-09-200-355-3
; Sequence 3, Application US/09200355
; Patent No. 6451524
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/09/200,355
; CURRENT FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 201
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-200-355-3

Alignment Scores:
Pred. No.: 2,2e-09 Length: 201
Score: 105.00 Matches: 19
Percent Similarity: 95.00% Conservative: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 3 Gaps: 0

US-09-632-036F-42 (1-20) x US-09-200-355-3 (1-201)

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RESULT 2

US-09-146-283-3
; Sequence 3, Application US/09146283
; Patent No. 5976546
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Compositions
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,283
; FILING DATE: 03-SEPT-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2385 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; INDIVIDUAL ISOLATE: GM-CSF-HER-2 fusion gene; Fig. 8
US-09-146-283-3

Alignment Scores:
Pred. No.: 4,13e-08 Length: 2385
Score: 105.00 Matches: 19
Percent Similarity: 95.00% Conservative: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 2 Gaps: 0

US-09-632-036F-42 (1-20) x US-09-146-283-3 (1-2385)

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Db 1892 ATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAGGGGTGCCGCCGACGACGAGA 1951

RESULT 3

US-08-579-823A-3
; Sequence 3, Application US/08579823A
; Patent No. 6080409
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Ruegg, Curtis L.
; APPLICANT: Wu, Hongyu
; TITLE OF INVENTION: Immunostimulatory Composition and Method
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Ave. Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,823A
; FILING DATE: 03-DEC-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Judge, Linda R.
; REGISTRATION NUMBER: 42,702
; REFERENCE/DOCKET NUMBER: 7636-0010
; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 11, 2005, 00:00:23 ; Search time 391.818 Seconds
(without alignments)
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Title: US-09-632-036F-42

Perfect score: 114

Sequence: 1 INGTSCVDLDKCPAEQR 20

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Published Applications NA_Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	92.1	201	5	US-10-109-213-3
2	105	92.1	884	6	US-10-412-804A-7
3	105	92.1	1479	6	US-10-412-804A-1
4	105	92.1	2149	6	US-10-412-804A-9
5	105	92.1	2164	6	US-10-412-804A-5
6	105	92.1	2320	9	US-10-956-373-1
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8	105	92.1	3504	9	US-10-794-514A-329
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13	105	92.1	3768	3	US-09-854-356-9	Sequence 9, Appli
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15	105	92.1	3768	3	US-09-984-092-3	Sequence 3, Appli
16	105	92.1	3768	6	US-10-313-644-1	Sequence 1, Appli
17	105	92.1	3768	7	US-10-280-576-3	Sequence 3, Appli
18	105	92.1	3768	7	US-10-441-79C-3	Sequence 3, Appli
19	105	92.1	3768	7	US-10-384-339C-52	Sequence 52, Appli
20	105	92.1	4473	3	US-09-441-411-5	Sequence 5, Appli
21	105	92.1	4473	3	US-10-146-473-32	Sequence 32, Appli
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57	98	86.0	3955	3	US-09-751-708A-117	Sequence 117, App
58	98	86.0	3955	8	US-10-428-817A-113	Sequence 113, App
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62	81	71.1	151	8	US-10-484-067-12	Sequence 12, Appli
63	78	68.4	154	8	US-10-484-067-6	Sequence 6, Appli
64	78	68.4	828	8	US-10-484-067-3	Sequence 3, Appli
65	57	50.0	1167	7	US-10-282-122A-9291	Sequence 9291, Ap
66	56	49.1	1941	6	US-10-108-260A-2086	Sequence 2086, Ap
67	55	48.2	589	4	US-09-925-065A-537341	Sequence 537341, A
68	53	46.5	334	7	US-10-424-599-51731	Sequence 51731, A
69	52.5	46.1	2295	9	US-10-114-270-107	Sequence 107, App
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71	52.5	46.1	2674	9	US-10-956-157-2130	Sequence 2130, Ap
72	52	45.6	778	5	US-10-027-632-162468	Sequence 162468, A
73	52	45.6	778	6	US-10-027-632-162468	Sequence 162468, A
74	52	45.6	1467	10	US-11-097-143-13199	Sequence 13199, A
75	52	45.6	2846	10	US-11-097-143-13198	Sequence 13198, A
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77	51.5	45.2	1223197	5	US-10-027-632-179264	Sequence 179264, A
78	51.5	45.2	1223197	6	US-10-027-632-179264	Sequence 179264, A
79	51	44.7	602	4	US-09-925-065A-695694	Sequence 695694, A
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C 83      50.5      44.3 956 8 US-10-774-355A-824      Sequence 824, App
C 84      50.5      44.3 1915 4 US-09-925-065A-78681      Sequence 78681, A
C 85      50      43.9 349 8 US-10-425-115-123077      Sequence 123077,
C 86      50      43.9 369 7 US-10-282-122A-18540      Sequence 18540, A
C 87      50      43.9 369 7 US-10-282-122A-19114      Sequence 19114, A
C 88      50      43.9 1783 7 US-10-425-114-15485      Sequence 15485, A
C 89      50      43.9 2568 8 US-10-491-213-77      Sequence 77, Appl
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C 93      50      43.9 15425 5 US-10-091-504-1654      Sequence 1654, Ap
C 94      94      50      43.9 15425 6 US-10-227-577-1558      Sequence 1558, Ap
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C 96      50      43.9 43623 8 US-10-741-600-17818      Sequence 17818, A
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C 98      50      43.9 119501 6 US-10-174-319-15      Sequence 15, Appl
C 99      50      43.9 1230025 6 US-10-289-762-1      Sequence 1, Appli
C 100      49.5      43.4 553 5 US-10-027-632-266944      Sequence 266944,
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ALIGNMENTS

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US-10-109-213-3
; Sequence 3, Application US/10109213
; Publication No. US20020168670A1
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; TITLE OF INVENTION: Identification Of Disease Predictive Nucleic Acids
; FILE REFERENCE: IBIS0009
; CURRENT APPLICATION NUMBER: US/10/109,213
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US/09/200,355
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 201
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-109-213-3
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Alignment Scores:
Pred. No.: 3.13e-09      Length: 201
Score: 105.00      Matches: 19
Percent Similarity: 95.00%      Conservative: 0
Best Local Similarity: 95.00%      Mismatches: 1
Query Match: 92.11%      Indels: 0
DB: 5      Gaps: 0
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US-09-632-036F-42 (1-20) x US-10-109-213-3 (1-201)
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RESULT 2
US-10-412-804A-7
; Sequence 7, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 7
; LENGTH: 884
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (77)..(568)
US-10-412-804A-7

Alignment Scores:
Pred. No.: 1.62e-08      Length: 884
Score: 105.00      Matches: 19
Percent Similarity: 95.00%      Conservative: 0
Best Local Similarity: 95.00%      Mismatches: 1
Query Match: 92.11%      Indels: 0
DB: 6      Gaps: 0

US-09-632-036F-42 (1-20) x US-10-412-804A-7 (1-884)

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RESULT 3
US-10-412-804A-1
; Sequence 1, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
; APPLICANT: Tatarewicz, Suzanna
; TITLE OF INVENTION: HER-2 Receptor Tyrosine Kinase Molecules and Uses
; FILE REFERENCE: 01-1624-A
; CURRENT APPLICATION NUMBER: US/10/412,804A
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 60/371,912
; PRIOR FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1169)
; OTHER INFORMATION: "n" can be a, g, c, or t
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1170)
; OTHER INFORMATION: "n" can be a, g, c, or t
US-10-412-804A-1

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Score: 105.00      Matches: 19
Percent Similarity: 95.00%      Conservative: 0
Best Local Similarity: 95.00%      Mismatches: 1
Query Match: 92.11%      Indels: 0
DB: 6      Gaps: 0

US-09-632-036F-42 (1-20) x US-10-412-804A-1 (1-1479)

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Db      1321      ATCAACTGCACCCACTCTCTGTGTGGACCTGGATGACAGGGCTGCCCGCCGAGCAGAGA 1380
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RESULT 4
US-10-412-804A-9
; Sequence 9, Application US/10412804A
; Publication No. US20030228606A1
; GENERAL INFORMATION:
; APPLICANT: Jing, Shuqian
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GenCore version 5.1.6
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Title: US-09-632-036F-42
Perfect score: 114
Sequence: 1 INGTSCVDLDKGPAPQR 20

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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- 4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	85	74.6	149419	7	US-11-112-908-49
3	85	74.6	157224	7	US-11-112-908-51
4	85	74.6	161726	7	US-11-112-908-48
5	85	74.6	161726	7	US-11-112-908-52
6	54	47.4	159497	7	US-11-112-908-61
7	54	47.4	171427	7	US-11-112-908-60
8	48	42.1	882	6	US-10-750-185-39806
					Sequence 18, Appl
					Sequence 49, Appl
					Sequence 51, Appl
					Sequence 48, Appl
					Sequence 52, Appl
					Sequence 61, Appl
					Sequence 60, Appl
					Sequence 39806, A

Sequence 418, App
Sequence 49750, A
Sequence 317, App
Sequence 41, Appl
Sequence 5252, A
Sequence 55, Appl
Sequence 48688, A
Sequence 85, Appl
Sequence 28, Appl
Sequence 16, Appl
Sequence 5, Appl
Sequence 50776, A
Sequence 36037, A
Sequence 61, Appl
Sequence 42547, A
Sequence 61950, A
Sequence 42585, A
Sequence 24808, A
Sequence 58741, A
Sequence 33376, A
Sequence 54843, A
Sequence 44139, A
Sequence 11, Appl
Sequence 5, Appl
Sequence 211, App
Sequence 30, Appl
Sequence 31, Appl
Sequence 1513, Ap
Sequence 2, Appl
Sequence 3, Appl
Sequence 3374, Ap
Sequence 3382, Ap
Sequence 1615, Ap
Sequence 43200, A
Sequence 57145, A
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Sequence 135, App
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Sequence 43, Appl
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Sequence 59, Appl
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Sequence 31742, A
Sequence 37922, A
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Sequence 19133, A
Sequence 43395, A
Sequence 31530, A
Sequence 54605, A
Sequence 38658, A
Sequence 59181, A
Sequence 43108, A
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Sequence 63378, A
Sequence 61216, A
Sequence 35975, A
Sequence 55608, A
Sequence 26035, A
Sequence 64852, A
Sequence 29, Appl
Sequence 30, Appl
Sequence 26, Appl

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C 82 41 36.0 151169 7 US-11-121-086-38 Sequence 38, Appl
C 83 41 36.0 158632 7 US-11-121-086-30 Sequence 30, Appl
C 84 41 36.0 159695 7 US-11-121-086-56 Sequence 56, Appl
C 85 41 36.0 160170 7 US-11-121-086-32 Sequence 32, Appl
C 86 41 36.0 160213 7 US-11-121-086-103 Sequence 103, Appl
C 87 41 36.0 166020 7 US-11-112-908-28 Sequence 28, Appl
C 88 41 36.0 171247 7 US-11-112-908-27 Sequence 27, Appl
C 89 41 36.0 171936 6 US-10-933-025-24 Sequence 24, Appl
C 90 41 36.0 182190 7 US-11-121-086-102 Sequence 102, Appl
C 91 40.5 35.5 169047 7 US-11-121-086-15 Sequence 15, Appl
C 92 40 35.1 1102 6 US-10-909-125-1370 Sequence 1370, Ap
C 93 40 35.1 110 6 US-10-909-125-21 Sequence 21, Appl
C 94 40 35.1 600 6 US-10-750-185-786 Sequence 786, App
C 95 40 35.1 600 6 US-10-750-185-2013 Sequence 2013, Ap
C 96 40 35.1 1056 6 US-10-750-185-43622 Sequence 43622, A
C 97 40 35.1 1062 6 US-10-750-185-55567 Sequence 55567, A
C 98 40 35.1 1199 6 US-10-750-185-47104 Sequence 47104, A
C 99 40 35.1 1223 6 US-10-750-185-63683 Sequence 63683, A
C 100 40 35.1 1326 6 US-10-750-185-32911 Sequence 32911, A
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ALIGNMENTS

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US-10-770-726-18
; Sequence 18, Application US/10770726
; Publication No. US20050266409A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; FILE REFERENCE: AM101079 (031896-010000)
; CURRENT APPLICATION NUMBER: US/10770,726
; CURRENT FILING DATE: 2004-02-04
; NUMBER OF SEQ ID NOS: 48640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 4530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-770-726-18
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Alignment Scores:
Pred. No.: 2.02e-07 Length: 4530
Score: 105.00 Matches: 19
Percent Similarity: 95.00% Conservative: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.11% Indels: 0
DB: 6 Gaps: 0
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US-09-632-036F-42 (1-20) x US-10-770-726-18 (1-4530)
Qy 1 IleAsnGlyThrHisSerCysValAspLeuAspAspLysGlyCysProAlaGluGlnArg 20
Db 2032 ATCAACTGCACCCACTCTGTGTGGACCTGGATGACAAGGGCTGCCCGCCGACGACGAGA 2091
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RESULT 2
US-11-112-908-49
; Sequence 49, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
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; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 49
; LENGTH: 149419
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-49
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Pred. No.: 0.0271 Length: 149419
Score: 85.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.56% Indels: 0
DB: 7 Gaps: 0
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US-09-632-036F-42 (1-20) x US-11-112-908-49 (1-149419)

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Qy 6 SerCysValAspLeuAspAspLysGlyCysProAlaGluGlnArg 20
Db 13921 AGCTGTGTGGACCTGGATGACAAGGGCTGCCCGCCGACGACGAGA 13965
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RESULT 3
US-11-112-908-51
; Sequence 51, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 51
; LENGTH: 157224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-51
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Score: 85.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 74.56% Indels: 0
DB: 7 Gaps: 0
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US-09-632-036F-42 (1-20) x US-11-112-908-51 (1-157224)
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RESULT 4
US-11-112-908-48
; Sequence 48, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
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